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54 16 AAR64213 Urinary plasm. 34 100.0 246 22 AAV991073 C glutamicum 34 100.0 246 20 AAV93344 Mutant human 34 100.0 246 20 AAV933122 Human urinary 34 100.0 246 20 AAV933123 Human urinary 34 100.0 246 20 AAV933124

ALIGNMENTS

Urea plasminogen activator residues 177-184.

AAR74920;

13-MAY-1996 (first entry)

AAR74920 standard; Peptide; 8 AA

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Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent. t-PA; tissue plasminogen activator; urea plasminogen activator; UK; variant; fibrin specificity; haemorrhagic tendency. WPI; 1995-155249/20. 01-OCT-1993; 29-JUL-1994; 30-SEP-1994; W09509908-A1 Homo sapiens. 13-APR-1995. Negoro T, (SUMU) SUMITOMO SEIYAKU KK. Sato H; 93JP-0269983. 94JP-0197635. 94WO-JP01629

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AAR74919
               Query Match
Best Local S
Matches 6
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                    The urinary plasminogen activator (UK) residues 177-186 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 294-304. The UK replacement region at least contains the sequence of AAR74917. t-PA variants, having residues 280-304 substituted with the corresponding residues from UK, have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                                                            Sequence
                                                                                                                                                                                                                                                Claim 3; Page 37; 64pp; Japanese.
                                                                                                                                                                                                                                                                               Tissue plasminogen activator (t	ext{-PA}) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
                                                                                                                                                                                                                                                                                                                                WPI; 1995-155249/20
                                                                                                                                                                                                                                                                                                                                                                                          (SUMU ) SUMITOMO SEIYAKU KK. (SUMU ) SUMITOMO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993;
29-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t-PA; tissue plasminogen activator; urea plasminogen activator;
variant; fibrin specificity; haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urea plasminogen activator residues 177-186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR74919 standard; Peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4;
                                                                                                                                                                                                                                                                                                                                                              Negoro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemorrhagic tendency.
                                                                                                                         haemorrhagic tendency.
                 Local Similarity 100 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RHRGGS 6
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3 rhrggs 8
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                                                                                            10
                                                                                                                                                                                                                                                                                                                                                            Sato H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                              A.
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94JP-0197635.
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                             100.0%;
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100.0%; Pred. No. 4.3e+05;
Live 0; Mismatches 0;
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                 0;
                             Score 34;
Pred. No.
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                             ; DB 16;
. 0.91;
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                                         Length 10;
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                 Indels
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AAR74922
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                                                                                                                                                           AAR72873
                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
Urokinase; tissue plasminogen activator; PCR; primer; amplification;
thrombosis; blood.
                                             Urokinase
                                                                            06-DEC-1995
                                                                                                            AAR72873;
                                                                                                                                       AAR72873 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     The urinary plasminogen activator (UK) residues 173-184 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 290-302. The UK replacement region at least contains the sequence of AAR74917. t-PA variants, having residues 280-304 substituted with the corresponding residues from UK, have improved fibrin specificity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-155249/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1993;
29-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urea plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                      corresponding residues from UK, have are useful in treatment of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                t-PA; tissue plasminogen activator; urea plasminogen variant; fibrin specificity; haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                           haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Negoro T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9509908-A1.
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7 rhrggs 12
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3 rhrggs 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Page 38; 64pp; Japanese.
                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato H;
                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; iconservative 0;
                                                                          (first entry)
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94JP-0197635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activator residues 173-183.
                                               fragment from amino acids 177-188.
                                                                                                                                           12
                                                                                                                                                                                                                                                                               ; Score 34; DB 1; Pred. No. 1.1; 0; Mismatches
                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                       improved fibrin specificity
s by reducing adverse reaction
                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                               Length 12;
                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                 0;
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AAR74927
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Best Local S
Matches 6
                                                                                                                                                                                                                                                         Urea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The peptides AAR72872-3 covering the amino acids (AA) 159-188 or 177-188 of urokinase (UK) were used to replace AA 276-306 of tissue plasminogen activator (t-PA)(AAR72874). The modified t-PA also has several N-bound sugar chain and additional consensus sequences replaced with urokinase sequences. The replacement was engineered by PCR using the primers AAQ86925-6 to replace the sequences encoding the AA 276-306 in the t-PA cDNA sequence. The modified t-PA may be used in the treatment of thrombosis and has an improved half-life in the blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator (t-PA) mutant comprising sequences of urinary plasminogen activator - has improved half life in the blood and may be used to treat thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                     t\text{-PA};\ tissue\ plasminogen\ activator;\ urea\ plasminogen\ activator;\ UK;\ variant;\ fibrin\ specificity;\ haemorrhagic\ tendency.
                                                                                                                                                                                                                                                                                                        AAR74927;
                                                                                                                                                                                                                                                                                                                              AAR74927 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 10; 13pp; Japanese.
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                                                                                                                                                                                                                                                                                  13-MAY-1996
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           WPI; 1995-155249/20.
                                  Negoro T,
                                                       (SUMU )
                                                                                         01-OCT-1993;
29-JUL-1994;
                                                                                                                           30-SEP-1994;
                                                                                                                                                   13-APR-1995
                                                                                                                                                                         WO9509908-A1
                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUMU ) SUMITOMO SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 100.0%;
Local Similarity 100.0%;
les 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                    1 RHRGGS 6
                                                                                                                                                                                                                                                                                                                                                                                        3 rhrggs 8
                                                                                                                                                                                                                                                                                                                                                     s
                                                                                                                                                                                                                                                         plasminogen activator
                                                       SUMITOMO SEIYAKU KK. SUMITOMO PHARM CO LTD
                                  Sato H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                               (first entry)
                                                                                         93JP-0269983.
94JP-0197635.
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                                                                                                                                                                                                                                                                                                                                Peptide;
                                                                                                                                                                                                                                                         residues 163-186.
                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 1.1;
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AAR42811
ID AAR
XX AAR
AC AAR
AC AAR
XX T1s
XX T1s
XX T1s
XX T1s
XX P1 Pep
FT P
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue plasminogen activator; t-PA; urinary plasminogen activator; u-PA; fibrin; fibrinogen; thrombolysis; thrombus; resistance; plasminogen activation factor inhibiting factor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The urinary plasminogen activator (UK) residues 163-186 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 280-304. The UK replacement region at least contains the sequence of AAR74917. t-PA variants, having residues 280-304 substituted with the corresponding residues from UK, have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                              Tissue plasminogen activator analog improved in fibrin specificity - obtd. by replacing part of aminoacid sequence with corresponding aminoacid sequence of urinary plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           u-PA (159-188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
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                        Claim 1-6; Page 25-26; 41pp; Japanese.
                                                                                                                                                          WPI; 1993-336902/42.
                                                                                                                                                                                                  Agui H,
                                                                                                                                                                                                                                              (SUMU)
                                                                                                                                                                                                                                                                                         03-APR-1992;
                                                                                                                                                                                                                                                                                                                                   03-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                              SUMITOMO PHARM CO LTD.
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                                                                                                                                                                                                  Negoro T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.
milarity 100.
Conservative
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10..20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                    Sato H, Sudo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "u-PA (159-188); claim 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "u-PA (159-180); claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "u-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "u-PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Japanese.
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Pred. No. 2.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (168-188);
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                                                                                                                                                                                                         Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 4"
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                                                                                                     Analogues of tissue plasminogen activator (t-PA) have amino acids from position 280-304 replaced by the corresponding sequence of urea plasminogen activator (UK). The UK replacement region at least contains the sequence of ARR74917. CS18 comprises a tPA variant (residues 276-306) where residues 294-304 have been replaced by the corresponding UK sequence. The t-PA variants have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-PA analogue has at least part of natural t-PA (276-306) substd. with corresp. amino acid sequence of u-PA (159-188). The analogue hardly causes activation of plasminogen (and hence decomposition of fibrinogen), while in circulation (blood). It activates plasminogen to cause thrombolyis when it reaches the locus of the thrombus where fibrin is present. It has high fibrin, and therefore thrombus specificity and is not expected to cause general bleeding as side effect. It also is resistant to plasminogen activation factor inhibiting factor 1. Therefore, the analogue will
                                                                                                                                                                                                                                                                Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1993;
29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t-PA; tissue plasminogen activator; urea plasminogen activator; UK; variant; fibrin specificity; haemorrhagic tendency.
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                                                              Seguence
                                                                                                                                                                                                                                 Example 3; Page 50; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                               WPI; 1995-155249/20.
                                                                                                                                                                                                                                                                                                                                            Negoro T, Sato H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           t-PA; tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be a safe thrombolytic agent
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Local Similarity 100.0%;
hes 6; Conservative (
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94JP-0197635.
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 Score 34;
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Pred. No.
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2.7;
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               Length 30;
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UK t-PA hybrid peptide CS16 residues 276-306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue plasminogen activator (t-PA) analogue - has increased fibrin specificity and can be used as an antithrombotic agent.
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 13-MAY-1996
                                   AAR76947;
                                                                  AAR76947 standard; Peptide;
                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-155249/20
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29-JUL-1994;
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variant; fibrin specificity; haemorrhagic tendency.
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                                                                                                                                                                                                                                                                                                                                                    haemorrhagic tendency.
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21 rhrggs
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SUMITOMO PHARM CO LTD
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                                                                                                                                                                                                                                                                                                               30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato H;
                                                                                                                                                                                                                            100.0%; Score 34; Dilarity 100.0%; Pred. No. 2. Conservative 0; Mismatches
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94JP-0197635
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                                                                                                                                                                                                                                                               DB 16;
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29-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analogues of tissue plasminogen activator (t-PA) have amino acids from position 280-304 replaced by the corresponding sequence of urea position activator (UK). The UK replacement region at least contains the sequence of AAR74917. CS15 comprises a tPA variant (residues the sequence of AAR74917. CS15 comprises a tPA variant (residues 276-306) where residues 290-302 have been replaced by the corresponding UK sequence. The t-PA variants have improved fibrin specificity and are useful in treatment of thrombosis by reducing adverse reactions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue plasminogen activator (t-PA) analogue - has increased specificity and can be used as an antithrombotic agent.
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                                     16-JUL-1993;
                                                                                                                                                JP07075580-A
                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                       Urokinase; tissue plasminogen activator; PCR; primer; amplification; thrombosis; blood.
                                                                                                                                                                                                                                                                            Urokinase
                                                                                                                                                                                                                                                                                                               06-DEC-1995
                                                                                                                                                                                                                                                                                                                                                       AAR72872
                                                                                                                                                                                                                                                                                                                                                                                      AAR72872 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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(SUMU ) SUMITOMO SEIYAKU KK
                                                                      28-DEC-1993;
                                                                                                             20-MAR-1995.
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                                                                                                                                                                                                                                                                            peptide
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94JP-0197635
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                                     93JP-0199101.
                                                                        93JP-0354355
                                                                                                                                                                                                                                                                            fragment from amino acids 159-188
                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No.
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2.7;
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Query Match

100.0%;

Score 34;

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16;

Length

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SXCCCCCCX PX PPX DXX PXX RXX

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RESULT
AAR7166
ID AA
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Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The peptides AAR72872-3 covering the amino acids (AA) 159-188 or 177-188 of urokinase (UK) were used to replace AA 276-306 of tissue plasminogen activator (t-PA)(AAR72874). The modified t-PA also has several N-bound sugar chain and additional consensus sequences replaced with urokinase sequences. The replacement was engineered by PCR using the primers AAQ86925-6 to replace the sequences encoding the AA 276-306 in the t-PA cDNA sequence. The modified t-PA may be used in the treatment of thrombosis and has an improved half-life in the blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue plasminogen activator (t-PA) mutant comprising sequences of urinary plasminogen activator - has improved half life in the blood and may be used to treat thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Sequence
                           t-PAs can be used bleeding.
                                         AAR79104 is the wild type plasminogen activator (t-PA), residues 276-306. By replacing these residues with the urint plasminogen activator (UK) sequences described in AAR71662-R71666, the fibrinogen specificity of t-PA is increased. The modified t-PAs can be used in the treatment of thrombosis and low systemic
                                                                                                                           Claim 1; Page 8; 10pp; Japanese
                                                                                                                                                      Novel modified tissue plasminogen activator - plasminogen activator peptide fragment
                                                                                                                                                                                                   WPI; 1995-117856/16.
                                                                                                                                                                                                                                                         28-JUL-1993;
                                                                                                                                                                                                                                                                                    28-JUL-1993;
                                                                                                                                                                                                                                                                                                                 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                             JP07039374-A
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                Modified urinary plasminogen activator; residues 159-188; tissue plasminogen activator; high fibrin specificity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified urinary plasminogen activator residues 159–188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1995
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                                                                                                                                                                                                                            (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 rhrggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RHRGGS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conserv
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ilarity 100.0%;
Conservative C
30
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                                                                                                                                                                                                                                                                                                                                                                                                     systemic bleeding.
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Pred. No. 2.7
D; Mismatches
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2.7;
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AAR64211
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                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
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Matches
                                                                                                                                                                                                                                         The urokinase sequence was used in a contruct for a novel tissue plasminogen activator (tpA) having amino acids 276-306 of tpA substituted by this urokinase sequence. The tpA analogue has resistance to inhibition by plasminogen activator inhibitor (PAI) while retaining its tpA activity. The analogue can be used in a drug for the treatment of thrombosis.
         t-PA; tissue plasminogen activator; urinary plasminogen
variant; fibrin specificity; haemorrhagic tendency.
                                    Urinary plasminogen activator residues 150-188
                                                                                          AAR64211 standard;
                                                                                                                                                                                                                       Sequence
                                                       13-MAY-1996
                                                                          AAR64211;
                                                                                                                                                                                                                                                                                                          Claim 1; Fig 6; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-214121/26.
N-PSDB; AAQ25737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urokinase fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR24949;
                                                                                                                                                                                                                                                                                                                          New tissue plasminogen activator analogue - is resistant inhibitor but retains properties of natural t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                 (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                        21 rhrggs 26
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                                                                                                                                                   1 RHRGGS 6
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ilarity 100.0%;
Conservative (
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                                                                                          Peptide;
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                                                                                          39 AA
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Pred. No.
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                 activator;
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The urinary plasminogen activator (UK) residues 159-203 are
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RESULT 14
AAR64212
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                              Novel t-PA variant containing urinary plasminogen activator residues - has improved fibrin specificity to reduce adverse reaction of haemorrhagic tendency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The urinary plasminogen activator (UK) residues 150-188 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 266-306. t-PA variants, having residues 276-306 substituted with the corresponding residues from UK, have improved fibrin specificity. They are useful in reducing adverse reactions of haemorrhagic tendency. Residues 266-275 and/or 307-321 are opt. substd..
Claim 4; Page 9; 15pp; Japanese. .
                                                                                                                                                                                                                                                                      JP06327473-A.
                                                                                                                                                                                                                                                                                                                                       t-PA; tissue plasminogen activator; urinary plasminogen activator; UK; variant; fibrin specificity; haemorrhagic tendency.
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                                                                                                    WPI; 1995-047896/07.
                                                                                                                                                                                                                                      29-NOV-1994.
                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                   (SUMU ) SUMITOMO SEIYAKU KK.
                                                                                                                                                                     19-MAY-1993;
                                                                                                                                                                                                      19-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 rhrggs 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RHRGGS 6
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RESULT 15
AAR64213
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue plasminogen activator (t-PA) variant to replace t-PA residues 266-306. t-PA variants, having residues 276-321 substituted with the corresponding residues from UK, have improved fibrin specificity. They are useful in reducing adverse reactions of haemorrhagic tendency. Residues 266-275 and/or 307-321 are opt. substd..
                                                                                                                                                                                              The urinary plasminogen activator (UK) residues 150-203 are used in a tissue plasminogen activator (t-PA) variant to replace t-PA residues 266-321. t-PA variants, having residues 276-306 substituted with the corresponding residues from UK, have improved fibrin specificity. They are useful in reducing adverse reactions of haemorrhagic tendency. Residues 266-275 and/or 307-321 are opt. substd..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t-PA; tissue plasminogen activator; urinary plasminogen activator; UK;
variant; fibrin specificity; haemorrhagic tendency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urinary plasminogen activator residues 150-203.
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                                                                                                                                                                                                                                                                                                                                                           Novel t-PA variant containing urinary plasminogen activator residues - has improved fibrin specificity to reduce adverse reaction of haemorrhagic tendency
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-047896/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1993;
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                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                         Claim 5; Page 9; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUMU ) SUMITOMO SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-1993;
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21 rhrggs 26
1 RHRGGS 6
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30 rhrggs 35
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                                                                       100.0%;
milarity 100.0%;
Conservative 0,
                                                                                                                                                                  54 AA;
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Pred. No. 4.1;
                                                                       Score 34; DB 16; Length 54; Pred. No. 4.9; , Mismatches 0; Indels
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Search completed: March 18, 2002, 09:48:55 Job time: 364 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1 RHRGGS 6
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US-08-560-098A-45
US-08-560-098A-45
US-08-560-098A-44
US-08-967-024C-25
US-08-967-098A-48
US-09-181-816-1
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US-08-560-098A-47
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Sequence 73, Appl
Sequence 45, Appl
Sequence 46, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 44, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 11, Appl
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18, Appl
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48, Appl
   Query Match
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TOPOLOG MOLECULE MOLECULE MYPOTHETI ANTI-SENS FRAGMENT ORIGINAL ORGANIE MS-07-942-1578	ATTORNEY/ NAME: REGISTR REFEREN TELECOMOUT TELEPHO TELEFAX INFORMATION SEQUENCE LENGTH: TYPE: TYPE: STRANDE	STAN	RESULT 1 US-07-942-157A- Sequence 1, A FATERIT NO. 56 GENERAL INFO APPLICANY: TITLE OF I TITLE OF I CORRESPOND ADDRESSE STREET: STREET: COTTY. 1	44444338743321 44444338743321 544321
TYPE: P CAL: NO SE: NO TYPE: N SOURCE: M: Homo	AGENT INF AGENT INF Pabst, Pa Pation NUM CCE/DOCKET NICATION NE: (404)8 : (404)8 : (404)8 : FOR SEQ FOR SEQ COARACTER COARACTER AMINO ACI DNESS: S	GEORGIA (C. USA 20309-4530 20309-4530 READABLE FORM: TYPE: Floppy RR: IBM PC con ING SYSTEM: PC	57A-1 1, Application 1, Application 1, Application 1, Application 1, Application 1, Expension 1, Expension 2,	30 88.2 1336 30 88.2 1336 30 88.2 1336 30 88.2 2337 30 88.2 2337 30 88.2 2337 30 88.2 2337 30 88.2 2337 30 88.2 2339 30 88.2 2339 30 88.2 2339 30 88.2 2339 31 88.2 2339 32 88.4 124 28 82.4 124 28 82.4 124 28 82.4 124 28 82.4 125 28 82.4 125 28 82.4 125 28 82.4 125 28 82.4 125
nal	ORMATION: TUTRE 1.284 BER: 31.284 'NUMBER: TSI108Cont. INFORMATION:)815-6508 15-6558 15-6555 ID NO: 1: LISTICS: LACIDS LACIDS	ORM: ppy disk compatible c-DOS/MS-DOS In Release #1.0, Version #1.25 DATA: R: US/07/942,157A 20908 435 ATA: ATA: ATA: ATA: ATA: ATA: ATA: ATA	Mer Inhibitor-Resistant Urokinase 3 S: 1ck & Cody tree Street Suite 2800	3 USS STORY
				Sequence 4, Appli Sequence 58, Appli Sequence 58, Appli Sequence 48, Appli Sequence 48, Appli Sequence 2, Appli Sequence 2, Appli Sequence 47, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 5, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 11, Appli Se

100.0%;

Score 34; DB 1;

JS-08-944-483-73

DDRESSEE:

JNTRY:

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INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
HOLECULE TYPE: NO. 6232456e
US-08-944-483-73
                                                                                                                                                            Ouery Match 100.0%; Score 34; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 17; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Becker Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
ELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
TORNEY/AGENT INFORMATION:
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US-08-560-098A-45
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Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/08560098A Patent No. 5976841
                                                                                                                                                                                                                                                                                                                                       Sequence 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/560
PRICH APPLICATION DATA:
17-NOV-1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: P 44 40 8
FILING DATE: 17-NOV-1994
ATTORNEY_AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE_DOCKET NUMBER: 148/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 628-88
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   Zent No. 59,000.
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CURRENT APPLICATION DATA:
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                                                                                                                                                                       APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acid
TYPE: amino acid
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITILE OF INVENTION: Proteins having Fibrinolytic and
TITILE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
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                            STATE.
COUNTRY: 20005
                                                                                            ADDRESSEE: Evenson, McKeown, Edwards & Lenahan STREET: 1200 G Street, N.W., Suite 700 CTTY: Mashington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Evenson, McKeown, Edwards & Lenahan STREET: 1200 G Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                 5, Application US/08560098A 5976841
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                                                           USA
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628-8844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P 44 40 892.7
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 254;
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RESULT 3 US-08-560-098A-49

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Matches
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                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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LENGTH: 306 amino acids
                                                                                                                                                                                        SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: ///
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FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA: 44 0 892.7
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
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NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                            APPLICATION NUMBER: US/08/560,0981
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P. 44 40 892.7
FILING DATE: 17-NOV-1994
                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      STREET: 1200 G STREET: Washington
                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LICANT: STEFFENS, Gerd Jose
LE OF INVENTION: Proteins h
LE OF INVENTION: Coagulatio
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5976841
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1200 G Street, N.W., Suite 700
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HEINZEL-WIELAND,
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                                                                                                                                                                     US/08/560,098A
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                    148/42448
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Best Local Similarity
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                                                                                                                                                                                                                                     NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 14
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8800
                                                                                                                                  TYPE: amino acids
TYPE: amino acids
TOPOLOGY: lin-
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE P
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
133 RHRGGS 138
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                          1 RHRGGS 6
                                                                        Similarity
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1200 G Street, N. W. Suite 700
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(202)628-8844
TD NO: 83:
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Pred. No. 22;
                                                                         Score 34;
Pred. No.
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                                                                                       DB 1; Length 365;
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US-08-720-012-83
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Best Local Similarity
Matches 6; Conser
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requence 83, Apr
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LENGTH: 365 amino acid
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APPLICATION NUMBER: US 08/093,741
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: CYANGE TOTAL
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                    133 RHRGGS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentTn BC1-
                                                                   TLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: EVANS, Joseph D
REGISTRATION NUMBER:
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               DDRESSEE:
                                                                                                                                                                              44, Application US/08560098A
o. 5976841
                                                                                                                                                             INFORMATION
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T: 1200 G Street, N. W. Suite 700
Washington, D.C.
RV. n c
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E: Evenson, McKeown, Edwards & Lenahan
1200 G Street, N.W., Suite 700
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                                                                                                       STEFFENS, Gerd Jose
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                       HEINZEL-WIELAND, Regina
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SCHNEIDER, JOHANNES
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SAUNDERS, DEREK J.
                                 ADDRESS:
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                                                                                                                                             r, Stephan
                                                     Proteins having Fibrinolytic and Coagulation-inhibiting Properties 60
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WNEARCH, Gerd APPLICANT: STEFFENS, Gerd APPLICANT: JANCCHA, Elke APPLICANT: HEINZEL-WIELANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION: Chimeric Proteins having Fibrinolytic
                                                                                                   CLASSIFICATION: 435
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                                                                                                                                           PPLICATION NUMBER:
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5. 6133011
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ATION NUMBER: (
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1200 G Street, N.W., Suite 700
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Stephan

Gerd Josef ELAND, Regina

US/08/967,024C

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TELEFAX: (202) 628-88 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                   NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER:
Local Similarity 100 es 6; Conservative
                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/UFILING DATE: 17-NOV-1995
                                                                                                                                                     amino acid
                                                                                                    TYPE:
                                                                                                                                                                                                                    (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                   linear
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                                                                                                                                                                                                                    628-8844
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                100.0%;
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                Score 34;
Pred. No.
                                 DB 2; Length 393;
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   Gaps
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Jian-Ning ich, Victor

PRO-UROKINASE MUTANTS

US/08/087,163

04353/003001

Score 34; Pred. No.

DB 1; Length 411; Indels

0 Gaps

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-967-024C-24
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                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-967-024C-25
                  Query Match
Best Local Similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 4
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,26
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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STATE: 20005
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                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14 PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORRESPONDENCE ADDRESS:
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: STEFFENS, Gerd Josef
PPLICANT: JANOCHA, Elke
PPLICANT: HEINZEL-WHIELAND, Regina
ITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
UMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RHRGGS 6
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1 RHRGGS 6
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                                                                                                                                                                                                                                                                   ELEPHONE:
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amino acid
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1200 G Street, N.W., Suite 700
                               100.0%; ilarity 100.0%; Conservative 0
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US-08-087-163-1
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US-08-286-748B-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
                                                                                APPLICANT: Victor Gui
TITLE OF INVENTION: (
TITLE OF INVENTION: (
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US, FILING DATE: 07/02/93 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
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les 6; Conserv
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o. 5759542
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                                                                                                                                                    Victor Gurewich
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SYSTEM: MS-DOS (Version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fish & Richardson
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COMPOSITIONS AND METHODS FOR THE DELIVERY OF DRUGS BY PLATELETS FOR THE TREATMENT OF

CARDIOVASCULAR AND OTHER DISEASES

26-APR-1990

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RESULT 13
US-08-153-799-18
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Best Local Similarity
Matches 6; Conserv
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CITY: Nurray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPITED:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0454
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
AFFICATION NUMBER:
FILING APPLICATION NUMBERS
                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/153,799

APPLICATION NUMBER: US/08/153,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 RHRGGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                 APPLICATION NUMBER: FILING DATE: 29-AP
APPLICATION NUMBER: PCT/GB90/00650
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STRANDEDNESS: sin
TOPOLOGY: linear
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LE OF INVENTION: Polypeptides
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                                                 GB 8909916.2
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Pred. No. 27;
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US-08-560-098A-48
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 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acid
                                                                                                                                                                                                                                       NAME: Swope, R Hain
REGISTRATION NUMBER: 92
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                   LENGTH: 411 amino acids TYPE: amino acid TOPOLOGY: linear
Local Similarity 100 es 6; Conservative
                                                                                                                                                                                                                        (908) 771 6159
                                                                                                protein
             100.0%;
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                 Score 34; DB 1; Length 411; Pred. No. 27;
 Mismatches
Gaps
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1 RHRGGS 6

0

ZIP: 20005

COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA: FILING DATE: 17-NOV-1994
ATTORNEY_AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 148
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800 TELEFAX: (202) 628-8844 INFORMATION FOR SEQ ID NO: 48: APPLICATION NUMBER: US/08/560,098/ FILING DATE: 17-NOV-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: P 44 40 892.7 ENERAL INFORMATION: SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELLAND, Regina
APPLICANT: STEFFENS, Gerd Josef
DITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties 179 RHRGGS 184 UMBER OF SEQUENCES: CITY: Washington STATE: DC TYPE: amino acid STRANDEDNESS: single ADDRESSEE: 597684 Application US/08560098A 2: Evenson, McKeown, Edwards & Lenahan 1200 G Street, N.W., Suite 700 411 amino acids USA linear protein 17-NOV-1994 Release #1.0, Version #1.30 (EPO) US/08/560,098A 148/42448

US-08-560-098A-48

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Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RHRGGS 6
| | | | | | | | |
| Db 179 RHRGGS 184

RESULT 15
US-09-181-816-1
US-09-181-816-1
| Sequence 1, Application US/09181816
| Patent No. 6277818
| GENERAL INFORMATION:
| APPLICANT: MAZAR Andrew P. APPLICANT: JONES, Terence R. ITILE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROXINASE
| TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROXINASE
| TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROXINASE
| TITLE OF INVENTION: PASHINGEN ACTIVATOR RECEPTOR
| FILE REFERENCE: 32904200300 SIDN 1-7
| CURRENT APPLICATION NUMBER: US/09/181,815
| CURRENT FILING DATE: 1998-10-29
| NUMBER OF SEQ ID NOS: 7
| SOPTWARE: Patentin ver. 2.0
| SEQ ID NOS: 17
| ORGANISM: Homo sapiems
| US-09-181-816-1
| Ouery Match 100.0%; Score 34; DB 4; Length 411;
| Best Local Similarity 100.0%; Pred. No. 27;
| Hatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
| Ouery Match 100.0%; Pred. No. 27;
| Hatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
| Organism: Homo sapiems 0; Ouery Matches 100.0%; Pred. No. 27;
| Hatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
| Ouery Match 18, 2002, 09:49:40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
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length: 2000000000
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34
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10.887 Million cell updates/sec
BLOSUM62
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Listing first 45 summaries
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pir2: *
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pir4: *
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88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2	88.2
342	304	286	284	284	284	284	284	276	276	276	276	275	275	275	274
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JN0542	G70300	R5SP2	C83237	A81661	A86571	C71507	F72055	T07531	A72250	B54547	S77499	S78273	T07361	T11810	S78397
head protein gp7 -	ribosomal protein	ribosomal protein	probable transcrip	ribosomal protein	L2 ribosomal prote	probable L2 riboso	ribosomal protein								

ALIGNMENTS

C;Species: Homo sapiens (man)
C;Date: 17-Dec-1992 *sequence_revision 04-Dec-1986 *text_change 15-Sep-2000
C;Date: 17-Dec-1992 *sequence_revision 04-Dec-1986 *text_change 15-Sep-2000
C;Accession: A00931; I52209; JT0102; A37561; I38102; S65783; A37562; A37563; A37564;
R;Riccio, A.; Grimaldi, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.
Nucleic Acids Res. 13, 2759-2771, 1985
A;Title: The human urokinase-plasminogen activator gene and its promoter.
A;Reference number: A00931; MUID:85215647 A;Cross references: GB:X02419; NID:g37601; PIDN:CAA26268.1; PID:g1834524
A;Note: the authors translated the codon ATG for residue 214 as Ile
A;Note: the authors translated the codon ATG for residue 214 as Ile
R;Nagamine, Y; Pearson, D, Grattan, M
Biochem, Biophys. Res. Commun. 132, 563-569, 1985
A;Title: Exon-intron boundary sliding in the generation of two mRNAs coding for porc
A;Reference number: 152209, MID:86050639
A;Accession: 152209 u-plasminogen activator (EC 3.4.21.73) precursor [validated] - human N;Alternate names: cellular plasminogen activator; urokinase; urokinase-type plasmin N;Contains: urokinase-type plasminogen activator chain A; urokinase-type plasminogen A; Molecule type: DNA A; Residues: 1-431 <RIC> A; Accession: A00931

preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 145-161 (NAGI) A; Residues: 145-161 (NAGI) A; Residues: 145-161 (NAGI) A; Residues: 145-161 (NAGI) A; Recoss-references: GB: K03027; NID: g340174; PIDN: AAA61257.1; PID: g340175 A; Nagai, M.; Hiramatsu, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, Gene 36, 183-188, 1985 Gene 36, 183-188, 1985 A; Recession: JRO 102; Molecular Clothing of cDNA coding for human preprourokinase.

A; Recession: JT0102; Molecular GDNA coding for human preprourokinase.

A; Recession: JT0102; Molecular GDNA coding for human preprourokinase. M.; Suyaı

A; Molecule type: mRNA
A; Residues: 1-213,'I,215-431 <NAG2>
A; Residues: 1-213,'I,215-431 <NAG2>
A; Residues: 1-213,'I,215-431 <NAG2>
A; Cross-references: GB: K03226; NID: g340155; PIDN: AAC9713B.1; PID: g340158; GB: D00244;
R; Verde, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Blasi, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 4727-4731, 1984
A; Title: Identification and primary sequence of an unspliced human urokinase poly(A)
A; Reference number: A37561; MUID: 84272706
A; Accession: A37561; MUID: 84272706

A; Molecule type: mRNA A; Residues: 66-431 <VER> A; Cross-references: GB:D00244; NID:g220138 R; Jacobb, P; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana, DNA 4, 139-146, 1985

E

DNA 4, 139-146, 1985
A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of human A;Reference number: I38102; MUID:85203359
A;Accession: I38102
A;Status: preliminary

A;Molecule type: mRNA A;Residues: 1-150,'W',152-213,'I',215-385,'C',387-429,'V',431 <JAC> A:Cross-references: EMBL:X02760; NID:g35297; PIDN:CAA26535.1; PID:g35298

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A;Gene: GDB:PLAU
A;Cross-references: G
A;Map position: 10q24
A;Introns: 19/3; 29/1
A;Introns: proteo
A;Pathway: fibrinoly9
C;Superfamily: urokin
                                                                                                                                                                                                                                                                                                  A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR R;Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Olej submitted to the Brookhaven Protein Data Bank, January 1994
A;Reference number: A6682; PDB:IURK
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, R;Spraggon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson submitted to the Brookhaven Protein Data Bank, July 1995
A;Reference number: A66058; PDB:ILMM
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 168-175;1 C;Comment: This enzyme is found in urine in a high molecular mass form, consisting C.Comment: Urokinase-type plasminogen activator proteolytically activates plasming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M. submitted to the Brookhaven protein Data Bank, July 1993 A;Reference number: A51255; PDB:1KUD A;Contents: annotation; conformation and disulfide bond assignments R;Li, X.; Smith, R.A.G.; Dobson, C.M. Biochemistry 31, 9562-9571, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 21-30,'X',34-38,'X',40-43 <KEN>
A;Residues: 21-30,'X',32,'X',34-38,'X',40-43 <KEN>
A;Residues: 21-30,'X',32,'X',34-38,'X',40-43 <KEN>
A;Residues: 21-30,'X',32,'X',34-38,'X',40-43 <KEN>
A;Note: identification of a fucose and attempt to determine its attachment site R;Rabbani S.A.; Desjardins, J.; Bell, A.W.; Banville, D.; Mazar, A.; Henkin, J. Biochem. Biophys. Res. Commun. 173, 1058-1064, 1990
A;Title: An amino-terminal fragment of urokinase isolated from a prostate cancer A;Reference number: A36697; MUID:91097529
A;Accession: A36697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Molecule type: protein
A:Residues: 156-176;179-193,'T',195,'T',197-224 <SCH>
A:Residues: 156-176;179-193,'T',195,'T',197-224 <SCH>
R:Steffens: G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
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A;Title: The complete amino acid sequence of low molecular mass urokinase
A:Reference number: A37564; MUID:B3055099
A:Accession: A37564
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A; Residues: 21-177 <GUN>
R; Schaller, J; Nick, H; Rickli, E.E.; Gillessen, D.;
R; Schaller, J; Nick, H.; Rickli, E.E.; Gillessen, D.;
Eur. J. Biochem. 125, 251-257, 1982
A; Title: Human low-molecular-weight urinary urokinase.
A; Reference number: A37563; MUID:83003608
A; Accession: A37563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 21-34 < RAB> R; L1, X.; Bokman, A.M.; I
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A;Molecule type; mRNA
A;Residues: 21-140,'L',142-213,'I',215-431 <YOS>
A;Residues: 21-140,'L',142-213,'I',215-431 <YOS>
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A;Cross-references: EMBL.D1143; NID.g1311467; PIDN:BAA01919.1; PID:g119928
A;Garanter, W.A.; Steffens, G.J.; Ottlng, F.; Kim, S.M.A.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1155-1165, 1982
A;Title: The primary structure of high molecular mass urokinase from human urine.
A;Reference number: A37562; MUID:83055084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequential (1)H NNR assignments and secondary structure of the kringle A;Reference number: A44375; MUID:93003110
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Blochim. Blophys. Acta 193, 83-89, 1996
A;Title: Characterization of single chain urokinase-type plasminogen activator with a
A;Reference number: S65783; MUID:96186279
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                                                                        Description: proteolytically activates plasminogen
                                          fibrinolysis
   urokinase-type plasminogen activator;
                                                                                                                                                                                                          GDB:119497; OMIM:191840
                                                                                                                                         154/1; 227/2;
                                                                                                                                                                                                                                                                                                          2.5 angstroms, residues 168-175;179-426
igh molecular mass form, consisting of a
proteolytically activates plasminogen,
                                                                                                                                             277/1;
       EGF
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   homology; kringle homology;
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-433 <AUY
A; Residues: 1-433 <AUY
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C; Keywords: glycoprotein; heterodimer; Prodrolase; Kringle; serine proteinase
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F;178-431/Product: plasminogen activator chain B #status predicted <BCH>
F;167-298,208-24,216-287,315-384,347-363,374-402/Disulfide bonds: #status predicted
F;223,274,378/Active site: His, Asp, Ser #status predicted
F;223,274,378/Active site: His, Asp, Ser #status predicted
F;223,274,378/Active site: Asp, Ser #status predicted
F;223,274,378/Active site: Asp, Ser #status predicted
F;223,274,378/Active site: Asp, Ser #status predicted
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A;Title: Nucleotide and deduced amino acid A;Reference number: S14687; MUID:90287734
A;Rocession: S14687
A;Roleovia ****
R;Kraetzschmar, J.; Haendler, B.; Kojima, igene 125, 177-183, 1993
A;Title: Bovine urokinase-type plasminogen A;Reference number: JN0580; MUID:93216119
A;Accession: JN0560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               u-plasminogen activator (EC 3.4.21.73) precursor - yellow baboon C;Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999 C;Accession: $14657; 508651 C;Accession: $14657; 508651 R;Au, Y.P.T.; Wang, T.W.; Clowes, A.W. Nucleic Acids Res. 18, 3411, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: flbrinolysis; glycoprotein; heterodimer; hydrolase; kringle; serine prote F;1-20/Domain: signal sequence #status predicted <SIC>F;21-43/Product: urokinase-type plasminogen activator, single chain form #status pre F;21-17/Product: urokinase-type plasminogen activator chain A #status experimental <F;31-62/Domain: EGF homology <EGF>F;01-151/Domain: kringle homology <EGF>F;156-177/Product: urokinase-type plasminogen activator chain A1 #status experimental F;179-431/Product: urokinase-type plasminogen activator chain B #status experimental F;179-431/Product: urokinase-type plasminogen activator chain B #status experimental F;379-431/Product: urokinase-type plasminogen activator chain B #status experimental F;319-33-51,33-62,70-151,91-133,122-146,168-299,209-225,217-288,313-382,345-361,372 F;31-39,33-51,33-62,70-151,91-133,122-146,168-299,209-225,217-288,313-382,345-361,372 F;38-Minding site: carbohydrate (Thr) (covalent) #status experimental F;224,775,376/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                  u-plasminogen activator (EC 3.4.21.73) precursor - bovine N;Alternate names: upA C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_C;Accession: JN0560
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100.0%; Pred. No. 15;
:1ve 0; Mismatches C
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ision 31-Dec-1993 #text_change 16-Jul-1999
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adenosylhomocysteinase (EC 3.3.1.1) DKF2p564A1523 - N:Alternate names: protein DKF2p564A1523.1 C:Species: Homo sabiene /m-n
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6; Conserv
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; Fittle: cDNA and gene nucleotide sequence of porcine plasminogen activator; Reference number: A00932; MUID:85087954
; Accession: A00932
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;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
;1-20/Domain: signal sequence #status predicted <SIG>
;21-179/Product: plasminogen activator chain A #status predicted <MAI>
;21-179/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
;33-64/Domain: EGF homology <EGEF>
;72-153/Domain: Kringle homology <EGEF>
;72-153/Domain: Kringle homology <EGEF>
;73-163/Domain: Kringle Homology <EGEF>
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Date: 04-Dec-1986 *sequence_revision 17-Mar-1987 *text_change 07-Aug-1998
Accession: A00932
Nagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
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Experimental source: kidney cell line LLC-PK1
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r:wamputt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16469
A;Accession: T08681
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                                             A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1332 <WIL>
A; Cross-references: EMBL: 292789; PIDN:CAB07215.1; GSPDB:GN00022; CESP:H02I12.1
A;Cross-references: clone H02I12
                                                                                                                                             submitted to the EMBL Data Library, March 1997
A;Reference number: Z19656
A;Accession: T23024
A;Status; preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                 hypothetical protein H02I12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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A;Molecule type: mRNA
A;Residues: 1-1217 <GP
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R; Garel, A.A.; Delea
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C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
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C;Keywords: NAD; thioether hydrolase
F;379-408/Region: beta-alpha-beta NAD nucleotide-binding
F;244,278/Active site: Cys #status predicted
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C;Accession: T08681
A; Introns: 12/3; 29/1; 60/3; 246/1; 449/1; 756/1; 849/1; 961/1; 1103/3; 1214/3
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                                                                                                                                                                                                                                                C; Accession:
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A; Accession: S52714
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A;Residues: 1-597 <WAM>
A;Cross-references: EMBL:AL049954
                                      A;Gene: CESP:H02I12.1
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probable C2H2-type zinc finger protein [imported] - Arabidopsis thaliana (:Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change 02-Feb-2001 C;Accession: C84688 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 02-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 02-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Kaul, S.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Rounslev C D . Charter 03-Feb-2001 R;Lin, X.; Rounslev C . Charter 03-
                                                                                                                                                               RESULT
C84688
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A;Residues: 1-86 <BEC>
A;Cross·references: GB:L05062; NID:g304570; PIDN:AAA28287.1;
A;Cxperimental source: venom gland
C;Superimentaly: scorpion neurotoxin
C;Superimely: scorpion neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Becerril, B.; Vazquez, A.; Garcia, C.; Corona, M.; Bolivar, F.; Possani, L.D. Gene 128, 165-171, 1993
A;Title: Cloning and characterization of cDNAs that code for Na+-channel-blocki A;Reference number; JN0669; MUID:93292983
A;Accession: JN0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Na+-channel-blocking toxin (clone cngtIV) precursor - scorpion (Centruroides noxius) C;Species: Centruroides noxius C;Species: Centruroides noxius C;Detate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999 C;Accession: JN0671
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A;Molecule type: protein
A;Residues: 1-64 <POS>
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Blochem. J. 229, 739-750, 1985
A;Title: Scorpion toxins from Centruroldes noxius and
A;Reference number: S32789; MUID:86025386
A;Accession: S32789
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;Species: Centruroides noxius
;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
;Accession: S32789
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conser
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86/Product: Na+-channel-blocking toxin (clone cngtIV) *status
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1; Mismatches
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C; Species: Ps
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C; Accession:
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: C84688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <570>
A;Residues: 1-156 <570>
A;Status: preliminary; translated from GB/EMBD/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-310 <YOS>
A;Cross-references: EMBL:D89241; NID:g1749689; PIDN:BAA13902.1; PID:g1749690
A;Experimental source: strain PR745
                                                                                                     R;YOShloka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H. DNA RES. 4; 363-369, 1997
DNA RES. 4; 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs A;Reference number: 217323; MUID:98162722
A;Reference T43147
A;Accession: T43147
                                                                                                                                                                                                                           hypothetical protein - fission yeast (Schizosaccharomyces pombe)
c;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43147
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Nature 406, 959-964, 2000
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A;Gene: At2g28710
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Matches 5; Conserv
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Best Local Similarity 83:
Matches 5; Conservative
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ce: strain PAO1
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83.3%;
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A.; Larbig,
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||||||: 76 RHRGGA

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Query Match
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                                                                                                               Superfamily: toluene dioxygenase terminal oxygenase component large (Repwords: 2Fe-2S) aromatic hydrocarbon catabolism; metalloprotein; cfs-113/Domain: Risske [ZFe-2S] bomology CRSK>
75,77,95,98/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (coval
                                                                                                                                                                                                                                                     Residues: 1-431 <SHE>
(Cross-references: GB:AF060489
Experimental Source: strain CB3
Comment: This protein is the initial dioxygenase large (alpha) subunit in the carbazol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sene: prov
Sene: prov
Stepeorfamily: unassigned ATP-binding cassette proteins; ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irbazole dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain carAa -
Species: Sphingomonas sp.
Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18080.1; PID:e12646: Experimental source: strain H37Rv
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Residues: 1-376 <COL>
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Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Title: Deciphering the biology of Mycobacterium Reference number: A70500; MUID:98295987
Accession: G70800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      accession:
                                                                                                                                                                                                                                                                                                                                                                                              epherd, J.M.; Lloyd-Jones, G.
hem. Blophys. Res. Commun. 247, 129-135, 1998
tle: Novel carbaxole degradation genes of Sphingomonas CB3: Sequence analysis, transference number: JW0098; MUID:98300296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atus: preliminary; nucleic acid sequence not shown; translation not shown
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217 KHRGGS 222
y Match 91.2%;
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hes 5; Conservative
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83.3%;
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Pred. No. 55;
1; Mismatches
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Pred. No. 62;
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Pred. No. 47;
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Search completed: March 18, 2002, 09:50:28 Job time: 237 sec
                                                                                                                                                                                                                                                             C; Superfamily: common tobacco sucrose transport protein
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Plant Physiol. 118, 1473-1480, 1998
A;Title: Characterization of source- and sink-specific sucrose/H+ symporters from A;Reference number: Z17991; MUID:99063785
                                                                                                                                                                Query Match
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Matches 5
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                                                                                                                                                                                                                                                                                                                                   Cross-references:
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                                                                                                                                                                                                                                                                                                                   Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Daucus carota (carrot)
Date: 20-Sep-1999 *sequence_revision 20-Sep-1999 *text_change 21-Jul-2000
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ce: cultivar N
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Pred. No. 71;
1; Mismatches
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Title: Perfect score: Sequence:

US-09-544-665-1 34 1 RHRGGS 6

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

March 18, 2002, 09:47:31;

Scoring table:

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SUMMARIES

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SCXI_CENNO
Y736_HAEIN
URAA_STRRE
URAL_HORUSE
RK2_NICUSE
RK2_NGUSE
RK2_HORUSE
RK2_FIVI
RK

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length: 0 length: 2000000000

Searched:

number 贸贸

of.

hits satisfying chosen parameters:

100059 segs, 36664827 residues

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is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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1 arabidopsis
5 epifagus vi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Methazia; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANG2_BOVIN STANDARD; PRT; 123 AA. P80929; O1-KOV-1997 (Rel. 35, Created) O1-KOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) NNGIOGENIN-2 (EC 3.1.27.-).
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RLZ_AQUPY
RLZ_AQUAE
RLZ_AQUAE
HEAD_BPP21
PHR_STRGR
CDS1_RAT
VCL_THECC
KOPP_RABIT
PULA_KLEAE
NHEA_MOUSE
NHEA_MOUSE
NHEA_RAT
NME4_HUMAN
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; B703B9839919FD2F CRC64;
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[1]
SEQUENCE FROM N.A.
MEDLINE-85215647; PubMed-2987867;
MEDLINE-85215647; PubMed-2987867;
Riccio A., Grimaldi G., Verde P., Sebastio Mariccio A., Andrewski, P., Andrewski, P., Mariccio A., Parids Res., 13:2759-2771(1985).
                                                                                                                                                                                                                                                                                                                 "The primary structure of high molecular mass urokinase furine. The complete amino acid sequence of the A chain.", Hoppe-Seyler's Z. Physiol. Chem. 363:1155-1165(1982).
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                                                                                                   MEDIINE-83055099; PubMed-6754572;
Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe L.;
"The complete amino acid sequence of low molecular mass urokinase from human urine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagai M., Hiramatsu R., Kaneda T.,
Nishida M., Suyama T.;
"Molecular cloning of cDNA coding
Gene 36:183-188(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLAU
MEDLINE-96000858; PubMed-8591045;
Spraggon G., Phillips C., Nowak U.K., Ponting C.P., Saunders
Dobson C.M., Stuart D.I., Jones E.Y.;
"The crystal structure of the catalytic domain of human
                                                                                                                                                                           Eur. J. Biochem. 125:251-257(1982)
[7]
                                                                                                                                                                                                                   characterization
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                                                                                                                                                                                                                                                        MEDLINE-83003608; PubMed-6749491;
Schaller J., Nick H., Rickli E.E., Gillessen D., Lergier
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84272706; PubMed-6589620;
Verde F. Stoppelli M.P., Galeffi P.,
"Identification and primary sequence
poly(A)+ RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86056954; PubMed-2415429;
Nagai M., Hiramatsu R., Kaneda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotechnology 3:923-929(1985).
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Steffens G.J., Heyneker H.L.;
"Cloning and expression of the gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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20-MAR-1987 (Rel. 04, Last sequence update)
20-MAR-1987 (Rel. 04, Last annotation update)
20-ROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC
                                                                                    from human urine.
Hoppe-Seyler's Z.
                                                                                                                                                                                                                "Human low-molecular-weight urinary urokinase.
characterization and preliminary sequence data
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                                                                                                                                                         SEQUENCE OF 158-410
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.55084; PubMed-6754569;
Steffens G.J., Otting
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                                                                                    Physiol. Chem. 363:1043-1058(1982)
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                                                         ANGSTROMS)
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VARIANT LEU-141.

RY MEDLINE-97337920; PubMed-9194591;
RA TUTKNEN B., Schmätt M., Schmälfeldt B., Trommler P., Hell W.,
Turknen B., Schmätt M., Schmälfeldt B., Trommler P., Hell W.,

Creutzburg S., Graeff H., Magdolen V.;

"Mutational analysis of the genes encoding urokinase-type plasminogen
rativator (upA) and its inhibitor PAI-1 in advanced ovarian cancer.";

Electrophoresis 18:686-689(1997).

C-!- FUNCTION: POPENT PLASMINGED RATIVATOR AND IS CLINICALLY USED FOR

C-!- FUNCTION: POPENT PLASMIN.

C-!- FUNCTION: POPENT PLASMIN.

C-!- CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN

C-!- CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN

C-!- SUBUNIT: FOUND IN HIGH HOLECULAR MASS FORMS. EACH CONSISTS

C-!- SUBUNIT: FOUND IN HIGH MOLECULAR MASS FORM CONTAINS A

C-!- SUBUNIT: FOUND IN HIGH MOLECULAR MASS FORM CONTAINS A

C-!- SUBUNITICAL: AVAILABLE UNDER THE NAME ABBOXINASE (ABBOTT). USED

C-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

C-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

C-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Solution structure of the kringle plasminogen activator.";
J. Mol. Rio.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-97218551; PubMed-9065988;
Conne B., Berczy M., Belin D.;
"Detection of polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature
[10]
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Oswald R.E., Bogusky M.J., Bamberger M., Smith R.A.G., Dobson C.N.
"Dynamics of the multidomain fibrinolytic protein urokinase from dimensional NRR.";
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Sawasaki Y., Hanada K.;
"Characterization of single chain urokinase-type plasminogen
activator with a novel amino-acid substitution in the kringle
structure.";
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MEDLINE=94149701; PubMed=8:
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Structure 3:681-691(1995).
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MEDLINE-93003110; PubMed-1
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78:973-973(1997).
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00130; KR; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; EGF_1; 1.
PROSITE; PS010022; EGF_1; 1.
PROSITE; PS01016; EGF_2; PALSE_NEG.
PROSITE; PS01016; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS00134; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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PROSITE; PS00134; TRYPSIN_SER; 1.
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Q05589; Q28209;

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1URK: 08-MAY-95
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1KDU; 31-OCT-93.
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6; Conserv
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IPR000561; EGF-like.
IPR000001; Kringle.
IPR001254; Trypsin.
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BY SIMILARITY.
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KRINGLE.
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      PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00130; KR; 1.
SMART; SM00020; TYP_SPc; 1.
PROSITE: PS00022; EGF_1; 1.
PROSITE: PS01186; EGF_2; FALSE_NEG.
PROSITE: PS00012; KRINGLE_1; 1.
PROSITE: PS00070; KRINGLE_2; 1.
PROSITE: PS50070; KRINGLE_2; 1.
PROSITE: PS50240; TRYPSIN_DS; 1.
PROSITE: PS50240; TRYPSIN_HIS; 1.
PROSITE: PS00115; TRYPSIN_HIS; 1.
PROSITE: PS00115; TRYPSIN_HIS; 1.
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SIGNAL
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EMBL: L03546: AAASIATO
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InterPro; IPR000561; EGF-like.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
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EMBL; X85801; CAA59796.1;
PIR; JN0560; JN0560.
HSSP; P00749; ILMW.
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UROKINASE-TYPE PLASMINOGEN A CHAIN A (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
EGF-LIKE.
KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.

; Serine protease; Glycoprotein; Zymogen.

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"Bovine urokinase-type plasminogen activator and its receptor: cloning and induction by retinoic acid."; Gene 125:177-183(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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01-NOV-1997 (Rel. 35, Last
UROKINASE-TYPE PLASMINOGEN
(U-PLASMINOGEN ACTIVATOR).
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-AORTLC endothellum;
MEDLINE-93216119; PubMed-8385052;
Kraetzschmar J., Haendler B., Kojima
Schleuning W.-D.;
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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CTISSUE-Thoracic aorta;

CTISSUE-Thoracic aorta;

XX MEDLINE-90287734; PubMed-2113276;

XX MEDLINE-9028774; PubMed-2113276;

XX MEDLINE-902874; PubMed-2113276;

XX MEDLINE-902876;

XX MEDLINE-902874; PubMed-2113276;

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CONFLICT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
MCBI_TaxID=9556;
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                                                        EMBL; x51935; CAA36200.1; -. PIR; S14687; UKBAY. HSSP; P00749; 1LMW. MEROPS; S01.231; -.
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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p16227;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
UROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECURSOR (EC.
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Similarity 100.
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Pred. No. 5.9;
D; Mismatches
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RESULT
UROK_PIG
           Query Match
Best Local S
Matches 6
SEQUENCE FROM N.A.

**TISSUE-Kidney;
MEDLINE-85087954; PubMed-6096832;
MEDLINE-85087950; Palmed-6096832;
Nagamine Y., Pearson D., Altus M.S., Rel
**CDNA and gene nucleotide sequence of po
**CDNA and gene nucleotide sequence of po
Nucleic Acids Res. 12:9525-9541(1984).

[2]
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SMART; SMO0181; EGF; 1.
SMART; SM00181; KR; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SP: 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00022; KGT_2; FALSE_NEG.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00021; KRINGLE_2; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LSR; 1.
SERIMINOGEN ACTIVATION; Hydrolase; Serims activatio
                                                                                                                                                                                                                                                                                                                                                                                                                                         20 MAR 1987 (Rel. 04, Created 13-AUG-1987 (Rel. 05, Last se 20-AUG-2001 (Rel. 40, Last ar UROKINASE-TYPE PLASMINOGEN ACTIVATOR).
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID-9823;
[1]
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InterPro;
Pfam; PF00
Pfam; PF00
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IPR001254;
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CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
EGF-LIKE.
KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
BY SIMILARITY.
BY SIM
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annotation update)
ACTIVATOR PRECURSOR
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Pred. No. 5.9
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porcine p
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Sus.
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                                                                               activator.";
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Best Local S
Matches 6
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SMART; SM00130; KR; 1.
SMART; SM00020; TYP_SPC; 1.
SMART; SM00020; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01012; KRINGLE_2; 1.
PROSITE; PS02070; KRINGLE_2; 1.
PROSITE; PS01013; TRYPSIN_DOM; 1.
PROSITE; PS01134; TRYPSIN_HS; 1.
PROSITE; PS01135; TRYPSIN_HSR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00051; kringle; Pfam; PF00089; trypsin;
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Submitted (DEC-1986)
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Nagamine Y.;
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                                           th 100.
Similarity 100.
6; Conservative
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IPR001254;
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F-like domain; Zymogen; Signal.
1 20 BY SIMILARITY.
21 442 UROKINASE-TYPE PLASMINOGEN ACTIVATOR
21 18 CHAIN A (BY SIMILARITY).
190 442 CHAIN B (BY SIMILARITY).
29 65 EGF-LIKE.
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51; EGF-like.
D1; Kringle.
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BY SIMILARITY.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.
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BY SIMILARITY.
                                                    Score 34; DE
Pred. No. 6;
D; Mismatches
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Neurotoxin;
SIGNAL
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxin.
InterPro; IPR001209; Toxin.
Pfam; PF00537; toxin_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ANIDATION.

MEDLINE-96119048; PubMed-8585086;

Vazquez A., Tapia J.V., Ellason W.K., Martin B.M., Lebreton F.,

Delepierre M., Possani L.D., Becerril B.;

"Cloning and characterization of the cDNas encoding Na+
channel-specific toxins 1 and 2 of the scorpion Centruroides noxius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CENNO STANDARD; PRT; STANDARD; PRT; STANDARD; PRT; STANDARD; O1-APR-1990 (Rel. 14, Created) STANDARD; PRT; STANDARD; PRT; STANDARD; O2-AGG-2001 (Rel. 40, Last annotation TOXIN 1 PRECURSOR (TOXIN II.14) (CN1).
                                                                                                                                                                                                                                                                    ProDom; PD000908;
SMART; SM00505; Kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S81093; AAB36085.2; -. PIR; S32789; S32789. HSSP; P01492; IVNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Possani L.D., Martin B.M., Svendsen I., Rode G.S., Erickson B.W. "Scorpion toxins from Centruroides noxius and Tityus serrulatus. Primary structures and sequence comparison by metric analysis."; Biochem. J. 229:739-750(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Centruroides noxius (Mexican scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 20-84.
MEDLINE-86025386; PubMed-4052021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxicon 33:1161-1170(1995).
[2]
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SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: BINDS TO SODIUM CHANNELS AND INHIBITS THE INACTIVATION OF THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMISSION SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                      PR00284; TOXIN.
PR00285; SCORPNTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215
                                                                                                                                                                                                                                            Sodium
  ₹
                                                                                                                                                                                                                                                                    8; Scorpion_toxin; 1.
Knotl; 1.
                                   19
59
64
79
        ₹
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY,
ANIDATION (G-85 PROVIDE AMIDE GROUP).
P -> T (IN REF. 2).
ABBC1EA742F17222 CRC64;
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Query Match Best Local S Matches 5

Similarity 5; Conserv

Conservative

91.2%; 83.3%;

Score 31; DB Pred. No. 4.8;

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Length 86 Indels

Mismatches

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Matches 5
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P45665;
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of cDNAs that code for Na(+)-channel-blocking toxins of the scorpion Centruroides noxius Hoffmann.", Gene 128:165-171(1931).

-i- FUNCTION: BINDS TO SODIUM CHANNELS AND INHIBITS THE INACTIVATION OF THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMISSION OF THE ACTIVATION SECRETED.

-i- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                              SMART; SM00505;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L05062; AAA28287.1; -. HSSP; P01494; 2SN3.
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Eukaryota; Metazoa; Arthropoda; Chelic
Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENNO
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00537;
PRINTS; PR0028
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                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                Neurotoxin;
                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possani L.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93292983; PubMed-8390386;
Becerril B., Vazquez A., Garcia C., Corona M., Bolivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-6878;
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                                                                                    1 RHRGGS 6
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PR00285; SCORPNTOXIN.
PD000908; Scorpion_tc
                                                                                                               Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                    IPR001219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
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43
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84
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                                                                                                                                                                                ium Channel inhibitor; Amidation; Signal.

19 BY SIMILARITY.
84 TOXIN CNCTIV.
83 BY SIMILARITY.
85 BY SIMILARITY.
66 BY SIMILARITY.
66 BY SIMILARITY.
67 BY SIMILARITY.
88 BY SIMILARITY.
89 BY SIMILARITY.
80 BY SIMILARITY.
81 AMIDATION (G-85 PROVIDE AMIDE GROUP)
82 APPOTENTIAL).
83 (POTENTIAL).
84 (POTENTIAL).
85 PROVIDE AMIDE GROUP)
85 PROVIDE AMIDE GROUP)
86 CROSS PROVIDE AMIDE GROUP)
87 CROSS PROVIDE AMIDE GROUP)
88 CROSS PROVIDE AMIDE GROUP)
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89 CROSS PROVIDE AMIDE GROUP)
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                                                                                                                            91.2%;
83.3%;
                                                                                                             Score 31; DB
Pred. No. 4.8;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND INHIBITS THE INACTIVATION BLOCKING NEURONAL TRANSMISSION
                                                                                                                            DB
1.8;
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01-NOV-1995
20-AUG-2001
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STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Mirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Goodayne J.D.,
Kerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Goodayne J.D.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Picks C.A., Goodayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus
Bacteria; Pr
Haemophilus.
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C., "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y736_HAEIN
P44849;
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000175; Na_neurotran_symport.
pfam; pF00209; SNF; 1.
pROSITE; pS00610; Na_NEUROTRAN_SYMP_1; 1.
pROSITE; pS00754; NA_NEUROTRAN_SYMP_2; FALSE_NEG.
pROSITE; pS00267; NA_NEUROTRAN_SYMP_3; 1.
prosite; pS0267; Na_Neurotran_SYMP_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCIENCE 269:496-512(1995).
-I- FUNCTION: PUTATIVE SODIUM-DEPENDENT TRANSPORTER.
-I- SUBCELIULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32757; AAC22395.1; TIGR; HI0736; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=727;
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74 RHRGGA
                            Н
                RHRGGS 6
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                                                         . Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                proteome
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Proteobacteria;
 79
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
L SODIUM-DEPENDENT TRANSPORTER HI0736.
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                      91.2%;
                                                                                                                                     55177
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                                                         Score 31; DB Pred. No. 30; 1; Mismatches
                                                                                                                                               POTENTIAL.
                                                                                                                                     5CC50526DE854BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                               Transmembrane; Symport;
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                                                                                       Length 508
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SMART; SM00382: AAA; 1.
PROSITE; PS01008; DNAA; 1.
DNA replication; DNA-binding; A
NP_BIND 344 351
SEQUENCE 643 AA; 71317 MW;
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Q9ZH76;
20-AUG-2001
20-AUG-2001
20-AUG-2001
                                                                                                                                       P52623;
01-OCT-1996;
01-OCT-1996;
15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF071023; AAD08806.1; -.
Interpro; IPR003593; AAA.
Interpro; IPR001957; Bac_DnaA.
Pfam; PF00308; bac_dnaA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces reticuli.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1999)
-!- FUNCTION: PLAYS A
                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                          UMPK.
                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Majka J., Jakimowicz D., Messer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TU45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-1926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNAA
SEQUENCE FROM TISSUE-Brain;
                                                                                                                                                                                                     URK1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2akrzewska-Czerwinska
                                                                                                                                                                                                                                                                                125 RHRGGA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interactions of the
                                                                                                                                                                                                                                                                                                          1 RHRGGS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INITED (JAN-1999) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION
OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION;
IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS.
(DNAA BOX): 5'-TPATO(C/A)A-3'. DNAA BINDS TO ATP AND TO
ACIDIC PHOSPHOLIPIDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE DNAA FAMILY.
                                                                                                                                                                                                                                                                                                                                       5; Conservative
               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                     STANDARD;
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces lividans initiator
                                                                                                                                                                                                                                                                                                                                       Score 31; DB 1; Pred. No. 38; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                            Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    rp (POTENTIAL).
DB9E173DF24758B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schrempf H., Lisowski M.
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                                                                                                                                                                                                     260 AA
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                                                                                                                                                                                                                                                                                                                                                                        Length 643;
                                                             Euteleostomi;
; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 5
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01-MAY-1991
30-MAY-2000
CHLOROPLAST
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P21434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                      EMBL;
                                                                                 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                              Zurawski G., Bottomley W., Whitfeld P.R.; "Junctions of the large single copy repending of the Jarge and Nicotiana debicoin of the genes for tNNAHLS and the ribosomal Nucleic Acids Res. 12:6547-6558(1984).
                                                                                                                                                                                                                                                                                                                                            Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L31783; AAB50568.1; -. MGD; MGI:98904; Umpk. InterPro; IPR001324; PRK. Pfam; PF00485; PRK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97108719; PubMed-8951040; Ropp P.A., Traut T.W.; "Cloning and expression of a cDNP
                                                                                                                                                                                              Nucleic Acids Res. 12:6547-6558(1984).
                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arch. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain."
                                                                                                                                                                                                                                                                                    MEDLINE-84297246; PubMed-6089120;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-4089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 RHRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RHRGG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h. Biochem. Biophys. 336:105-112(1996).
CATALYTIC ACTIVITY: ATP + URIDINE - ADP + UMP.
PATHMAY: PYRIMIDINE SALVAGE PATHWAY.
SIMILARITY: BELONGS TO THE URIDINE KINASE FAMILY.
                                      ; X00798; CAB52367.1; -. 
S07356; R5NT2D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  debney1 (Debney's tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%;
nilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 18, Created)
(Rel. 18, Last sequence update)
(Rel. 39, Last annotation update)
50S RIBOSOMAL PROTEIN L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336:105-112(1996)
ATP + URIDINE - A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a cDNA encoding uridine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB; Pred. No. 24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        080F1C82C59C80AC
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                                                                                                                     There are no rest
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                                                                                                                                                                                                                             proteins
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                                                                                                                                                                                                                                             and the inverted chloroplast DNA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                              S19
                                                                                                                                           restrictions
                                                                                                    isb-sib.ch/announce/
                                                                                                                                                                                                                                and
                                                                                                                                                           EMBL outstation
                                                                                                                                                             a collaboration -
MBL outstation -
                                                                                                                                                                                                                             d repeats
: sequence
d L2.";
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0
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PIR;

Mendel; 5309; NICde;rpl2;1.
InterPro; IPR002171; Ribosomal_L2
Pfam; PF00181; Ribosomal_L2; 1.

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Best Local
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                             RK2_SPIOL STANDARD: PRT; 271 AA.
P06509; Q9HHV0; Q9M3II;
01-JAN-1988 (Rel. 06, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 (RIBOSOMAL PROTEIN CS-L4).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                         SEQUENCE OF 1-19 FROM N.A.
MEDLINE-88203193; PubMed-3362671;
Thomas F., Massenet O., Dorne A.M., Briat J.F.,
"Expression of the rp123, rp12 and rps19 genes i
                                                                                                                                                                                                                                                                              STRAIN-CV. GEANT D'HIVER, AND CV. MONATOL;
MEDLINE-21187424; PubMed-11292076;
MEDLINE-21187424; PubMed-11292076;
Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
Herrmann R.G., Mache R.;
"The plastid chromosome of spinach (Spinacia oleracea): complete
nucleotide sequence and gene organization.";
Plant Mol. Biol. 45:307-315(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                      Yamaguchi K., Knoblauch K., Subramanian A.R.; "Complete identification of ribosomal proteins an organelle (chloroplast) ribosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 1-10. MEDLINE-04297246; PubMed=6089120; Zurawski G. Bottomley W., Whittield P.R.; "Junctions of the large single copy region in Spinacia oleracea and Nicotiana debneyi of the genes for trnahis and the ribosomal of the genes for trnahis and the ribosomal nucleic Acids Res. 12:6547-6558(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllades; Caryophyllales; Chenopodiaceae; Spinacia.
N.BI_TaxID-3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spinacia oleracea (Spinach).
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                                                                                                                                                       METHYLATION, AND PARTIAL SEQUENCE.
                                                                                                                                                                                   Nucleic
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 RHRGG 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
                                                                                                                                                                                  Acids Res. 16:2461-2472(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00467; RIBOSOMAL_L2; 1.
l protein; Chloroplast.
266 AA; 28901 MW; 8F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                          to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and the inverted repeats chloroplast DNA: sequence proteins S19 and L2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                          databases
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L2.";
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RESULT 13
RKZ_HORVU
ID RKZ_HORVU
ID PA1096
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
CHLORO
OC ENKATY
OC TITLL
OX NCBL_T
RN [1]
RN SEQUEN
RA Hess V
RA Boerne
RT 'Inefil
RT 'Inefil
CC This :
CC This 
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Best Loc
Matches
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STRAIN-CV. HAISA;
MEDLINE-95086380; Pub
Hess W.R. Hoch B., Z
Boerner T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RK2_HORVU
P41096;
01-FEB-1995
01-FEB-1995
01-FEB-1996
CHLOROPLAST
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INIT_MET
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     "Inefficient rpl2 splicing in barley mutants with ribosome-defic plastids.";
Plant Cell 6:1455-1465(1994).
-i- SIMILARITY: BELONGS TO THE L2P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare (Barley).
Chloroplast.
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ244023; CAB56543.3; -.
EMBL; AJ400848; CAB88803.1; -.
EMBL; X07462; CAA30345.1; -.
EMBL; S07918; R5SP2.
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  Pfam; PF00181; Ribosomal_L2; 1.
PROSITE; PS00467; RIBOSOMAL_L2; 1.
Ribosomal protein; Chloroplast.
SEQUENCE 273 AA; 30045 MW; 4C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002171; Ribosomal_L2.
Pfam; PF00181; Ribosomal_L2; 1.
PROSITE; PS00467; RIBOSOMAL_L2; 1.
Ribosomal protein; Chloroplast; Methylation
                                                                                                  EMBL; X78185; CAA55028.1; ALT_SEQ.
Mendel; 4044; HORvu;rpl2;1.
InterPro; IPR002171; Ribosomal_L2.
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50S RIBOSOMAL PROTEIN L2.
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; B8E06EC44FD93B63 CRC64;
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        4C204966ACB7DBE9 CRC64;
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Query Match Best Local Similarity

88.2%;

Score Pred

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Length 273;

RESULT 14 RK2_MAIZE

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Matches

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EMBL; X68563; CAA60399.1; A
EMBL; X68563; CAA60371.1; -
EMBL; X68563; CAA60371.1; -
EMBL; X62070; CAA43993.1; A
PIR; S10500; R52M2.
PIR; S17874; S17874.
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01-NOV-1990
01-FEB-1996
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NCBL_TaxID-4577;
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE-95395841; PubMed-7666415;
Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
"Complete sequence of the maize chloroplast genome: gene content of the species of divergence and fine tuning of genetic information transcript editing ";
J. Mol. Biol. 251:614-628(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90332419; PubMed-2377464; Kavousi M., Giese K., Larrinua I.M., Subramanian A.R.; Kavousi M., Giese K., Larrinua I.M., Subramanian A.R.; Nucleotide sequence and map positions of the duplicated maize (Zea mays) chloroplast ribosomal protein L2.*; Nucleic Acids Res. 18:4244-4244(1990).
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                                                                             Pfam; PF00181; Ribosomal_L2; 1.
PROSITE: PS00461; RIBOSOMAL_L2; 1.
RIBOSOMAL PROTECT: RIBOSOMAL_L2; 1.
RIBOSOMAL PROTECT: RNA editing.
RIBOSOMAL PROTECT: RNA editing.
SEQUENCE 273 AA; 30065 MW; BA65197231EA3CA0 CRC64;
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91367263; PubMed-1653905; Hoch B., Maier R.M., Appel K., Igloi G.L., "Editing of a chloroplast mRNA by creation Nature 353:178-180(1991)
                                                                                                                                        Mendel; 11440; ZEAma;rpl2;1.
InterPro; IPR002171; Ribosomal_L2.
Pfam; PF00181; Ribosomal_L2; 1.
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Chioroplast.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Byermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.
NCBI_TaxID=4530;
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EMBL; X15901; CAA33928.1;
EMBL; M22826; CAB25243.1;
EMBL; L40578; AAD15254.1;
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MEDLINE-89196901; PubMed-3240862;
MOON E., Wu R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M., Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q., Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.; "The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals."; amajor plastid DNA inversion during the evolution of the cereals."; mol. Gen. Genet. 217:185-194(1989).
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STRAIN-CV. NIPPONBARE;
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Gene 70:1-12(1988).
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MEDLINE-89364698; PubMed-2770692;
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Mendel; 5002
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PS00467; RIBOSOMAL_L2; 1.
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: March 18, 2002, 09:52:24
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   09xt70 oryctolagus
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016618 homo sapien
0201848 homo sapien
09ptn4 gallus gall
09ug84 homo sapien
017240 bombyx mori
04559 caenorhabdi
09pw44 gallus gall
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09pw46 gallus gall
09pum4 gallus gall
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09pw47 gallus gall
                                                                                                                                097587 oryctolagus
                                                                                                                                              Description
gallus
gallus
gallus
rattus
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                    Query Match 100.0%; Best Local Similarity 100.0%; Matches 6; Conservative 0;
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                                                       SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE;
MEDLINE=99057575; PubMed=9837780;
Reno C., Boykiw R., Martinez M.L., Hart D.A.;
"Temporal alterations in mRNA levels for proteinases and inhibitors and their potential regulators in the healing medial collateral
                                                                                                                                                                                                                     Oryctolagus cuniculús (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
1 RHRGGS 6
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Q69558
Q9V6Y6
0 Q41927
2 Q9Q0D0
2 Q9Q0C9
1 Q63730
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Q9X035
Q9YEE5
Q9V6R2
Q9GWM2
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Q9I6I1
Q9XMU4
Q9XIL2
Q9F2Q1
Q9F2Q1
Q69724
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Q54419
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                      Score 34; DB
Pred. No. 10;
); Mismatches
                                                          1BC7ED30E071A06D CRC64;
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Q9v6r2 drosophila Q9gwm2 leishmania Q9ri90 streptomyce Q54419 serratia ma

09w228 drosophila
059558 mycobacteri
09w6y6 drosophila
041927 arabidopsis
099060 herpes simp
09000 herpes simp
063730 rattus norv
09p663 neurospora
09y663 thermotoga
09yee5 aeropyrum p
09v6r2 drosophila

DB 6; 0;

Length 128; Indels

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Q9XT70;
01-NOV-1999
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Q15844; O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1996 (TrEMBLrel. 17, Last annotation update)
UROXINASE-TYPE PLASMINOGEN ACTIVATER (FRAGMENT)
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InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
Pfam; PP00051; Kringle; 1.
Pfam; PP00089; trypsin; 1.
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PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryotolagus.
                                                                                                                 Nagai M., Hiramatsu R., Kaneda T., Hayasuke N., Arimura H., Nishida M., Suyama T.; "Molecular cloning of CDNA coding for human preprourokinase."; Gene 36:183-188(1985).
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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NON_TER 214
SEQUENCE 214 AA;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UROKINASE-TYPE PLASMINOGEN ACTIVATOR (FRAGMENT).
SEQUENCE FROM N.A.
MEDLINE-96186279; PubMed-8652631;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-86056954; PubMed-2415429;
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RA Jacobs P., Cravador A., Loriau R., Brock RA van Elsen A., Herzog A., Bollen A.; RT Molecular cloning, sequencing, and exprehuman preprounchinase cuNA."; L. DNA 4:139-146(1985). C. C. SIMILARITY: TO SERINE PROTEASES, TRYP C. BMBL; X02760; CAA26535.1; T. BMBL; X02760; CAA26535.1; T. HSSP; P00749; IURK.
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Matches 6
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-1ike,
InterPro; IPR000001; Kringle,
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00052; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM00181; EGF; 1.
SMART; SM001002; EGF_1; 1.
PROSITE; PS00022; EGF_1; 1.
      EMBL; XOZ760; CAZ26535.1; -.
EMBL; XOZ760; CAZ26535.1; -.
HSSP; P00749; IURK.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000061; EGF-11ke.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
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CONFLICT
SEQUENCE
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Q16618;
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HSSP;
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                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
UROKINASE PRECURSOR (EC 3.4.99.26).
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PROSITE; PS00021;
PROSITE; PS50070;
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Sawasaki Y., Hanada
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NE PROTEASE FAMILY (S1).
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SMART; SM00020; TTYP_SFC; 1.
PROSITE: PS00022; EGE_1; 1.
PROSITE: PS00021; KRINGLE_1; 1.
PROSITE: PS00070; KRINGLE_2; 1.
PROSITE: PS00134; TRYPSIN_HIS; 1.
PROSITE: PS00135; TRYPSIN_SER; 1.
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SIGNAL 1 20 POTENTIAL.
CHAIN 21 431 UROKINASE.
SEQUENCE 431 AA; 48664 MW; 16082504B57AC18B
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01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-MAY-2000 (TIEMBLrel. 13, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                         Q90G84
Q90G84;
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                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 66.7 KDA PROTEIN (FRAGMENT).
DKFZP564A1523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RHRGGS 6
||||||
248 RHRGGS 25
                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
   SEQUENCE FROM N.A
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Similarity 100.
6; Conservative
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nilarity 100.
Conservative
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50547 MW;
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Pred.
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Pred. No.
                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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HSSP; P10760; 1B3R.
Interpro; IPR0010043; Ado_hcyase.
Interpro; IPR001220; Lectin_legB.
Interpro; IPR001220; Lectin_legB.
Pfam; PF00670; AdoHcyase; 1.
PROSITE; PS00738; ADOHCYASE_1; 1.
PROSITE; PS00739; ADOHCYASE_2; UNKNOWN_PROSITE; PS00307; LECTIN_LEGUME_BETA; UI
                                                                                                                                                                            045599 PRELIMINARY;
045599;
01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
H0Z112.1 PROTEIN.
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STRAIN-EUROPEAN 200X300; TISSUE-MEDIAN SILK GLAND;
STRAIN-EUROPEAN 200X300; TISSUE-MEDIAN SILK GLAND;
Garel A.A., Deleage G.G., Prudhomme J.J.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z48802; CAA88741.1;
EMBL; Z48802; CAA88741.1;
SEQUENCE 1217 AA; 123410 MW; 4C5789F87F6866DD CRC64;
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01-NOV-1996 (TrEMBLrel
01-NOV-1996 (TrEMBLrel
SERICINIB
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Q17240;
                                                                                   Eukaryota; Metazoa; Nematu
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bombyx mori (Silk moth).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea, Bombycidae; Bombyx.
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Wambutt R., F
McLay K.;
Submitted (MAR-1997)
                                                                                                                                                        Caenorhabditis elegans.
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                                              SEQUENCE FROM N.A.
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and Functional Expression of Novel N-type Ca2+ Channel
T Variants.";
J. Biol. Chem. 274:34566-34575(1999).
R EMBL; AE173015; AAD51818.1;
R InterPro; IPR000636; CatLon_chan_non_lig.
R InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
R InterPro; IPR001696; Na_channel.
R InterPro; IPR00207; Ca_channel.
RR InterPro; IPR002017; Ca_channel.
RR InterPro; IPR002011; Ca_channel_TrpL.
RR Pfam; PR00167; Channel_TrpL.
RR Pfam; PR00167; Channel.
RR Pfam; PR00167; NaCHANNEL.
RR PRINTS; PR00170; NACHANNEL.
RR PRINTS; PR00170; NACHANNEL.
RR PRINTS; PR00170; NACHANNEL.
RR PRINTS; PR00170; NACHANNEL.
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Best Local S
Matches 6
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownk
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watson A., werman, 2.2 Mb of contiguous
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TISSUE-DORSAL ROOT GANGLION NEURONS;
MEDILINE-200841702; PubMed-10574919;
Lu Q., Dunlap K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z92789; CAB07215.1; -.
InterPro; IPRO02557; Chitin_binding
Pfam; PF01607; Chitin_bind_2; 9.
SMARP; SM00494; ChtBD2; 12.
SEQUENCE 1332 AA; 145729 MW; 3D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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SEQUENCE FROM N.A.
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Local Similarity 100.
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Pred. No. 1.7
); Mismatches
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Pred. No. 1.1e+02;
Mismatches 0;
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1.7e+02;
thes 0;
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                                                                                                                                                                                                                                                                             Length 2146;
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J., Coulson
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Shownkeen
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ID Q9P446
ID Q9P446
DT 01-MAY
OC Eukary
OC Archos
OC GAILIUS
OC ARCHOS
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Matches 6
                          J. Biol. Chem. 0:0-0(1999).

EMBL; AF173017; AAD51820.1; -...
InterPro; IPR00036; Cattion_chan_non_lig.
InterPro; IPR001692; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002077; Cat_channel_TrpL.
Pfam; PP00520; ion_trans; 4.
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J. Biol. Chem. 0:0-0(1999).
EMBL; AF173019; AAD51822.1; -.
InterPro; IPR000656; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001696; Na_channel.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002111; Cat_channel_TrpL:
InterPro; IPR001111; Cat_channel_TrpL:
InterPro; IPR0011111; Cat_channel_TrpL:
InterPro; IPR001111; Cat_channel_TrpL:
InterPro; IPR001111; Cat_ch
                                                                                                                                                                                                                                                                                                                                            TESUENCE FROM N.A.
TISSUE-DORSAL ROOT GANGLION NEURONS;
Lu Q., Dunlap K.;
"Cloning and Functional Expression of
Variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B CDB6 VARIANT.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Q9PW44;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-TYPE CALCIUM CHANNEL ALPHA-1B CDB8 VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae
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PRINTS; PRO0170; NACHANNEL.
SEQUENCE 2157 AA; 245853 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9031;
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Similarity 100.0%;
6; Conservative 0
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Pred. No. 1.8e+02;
; Mismatches 0;
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; Galliformes; Phasianidae; Phasiani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR001896; Na_channel.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002011; Cat_channel_TrpL.
InterPro; IPR002111; Cat_channel_TrpL.
PRINTS; PR00167; CACHANNEL.
PRINTS; PR00170; NACHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSPOMS PRELIMINARY; PRT; 2182 AA.
OSPOMS;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-UN-2001 (TrEMBLrel. 17, Last annotation update)
O1-UN-2001 (TrEMBLRel. 17, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B CDB2 VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0170; NACHANNEL. SEQUENCE 2171 AA; 247055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last nnotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B CDB3 VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-DORSAL ROOT GANGLION NEURONS.
MEDLINE-20044702; PubMed-10574919;
     SEQUENCE FROM N.A. TISSUE-DORSAL ROOT GANGLION NEURONS
                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PUM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PUM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 274:34566-34575(1999).
EMBL; AF173013; AAD51816.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and Functional Expression of Novel N-type Ca2+ Channel Variants.";
                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                      Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RHRGGS 6
||||||
972 RHRGGS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RHRGGS 6 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q., Dunlap K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHRGGS 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity 100.0%;
6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.0%;
6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                      Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248259 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.
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Pred. No. 1.8
0; Mismatches
                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 13;
Pred. No. 1.8e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4023DD3D1AFA7EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1C34F9DF5991783E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT
Q9PW45
ID Q9
AC Q9
DT 01
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Best Local S
Matches 6
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Best Local Similarity 100.0%;
Matches 6; Conservative (
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InterPro; IPRO01682; Channel_pore_Ca_Na.
InterPro; IPRO01682; Channel_lore_Ca_Na.
InterPro; IPRO02077; Ca_channel.
InterPro; IPRO02111; Cat_channel_TrpL.
InterPro; IPRO02111; Cat_channel_TrpL.
InterPro; PRO0167; CACHANNEL.
PRINTS; PRO0167; CACHANNEL.
PRINTS; PRO0170; NACHANNEL.
SEQUENCE 2321 AA; 262972 MW; E6FB22:
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Q9TTA4;

Q9TTA4;

Q1-MAY-2000 (TrEMBLrel. 13, Created)

Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)

N-TYPE CALCIUM CHANNEL ALPHAIB SUBUNIT.
Q9PW45;
Q9PW45;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wrexpression of cloned alphalB, beta2a, a produces non-inactivating calcium channels bowine chromaffin cells.";
J. Neurosci. 0:0-0/2000.
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Lu Q., Dunlap K.;
"Cloning and Functional Expression of
"Variants";
J. Biol. Chem. 274:34566-34575(1999).
EMBL; AF173014; AAD51817.1;
                                                                                                                                                                                                                                                                                                     PRINTS; PRO0167; CACHANNEL.
PRINTS; PRO0170; NACHANNEL.
SEQUENCE 2331 AA; 260560 MW;
                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR000636; Cation_chan_non_lig.
InterPro: IPR001682; Channel_pore_Ca_Na.
InterPro: IPR001696; Na_channel.
InterPro: IPR002077; Ca_channel.
InterPro: IPR002117; Ca_channel_TrpL.
Pfam; PF00520; ion_trans; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Neurosci. 0:0-0(2000).
EMBL; AF173882; AAF24229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                  962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          947 RHRGGS 952
                                                                                                                              1 RHRGGS 6
| | | | | | |
962 RHRGGS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RHRGGS 6
                                                                       15
                                                                                                                                                                                                          Similarity 100.
6; Conservative
                                                                                                                                  967
  (TrEMBLrel. 13,
                                      PRELIMINARY;
                                                                                                                                                                                                                           100.0%;
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Channel_pore_Ca_Na.
                                                                                                                                                                                                            0
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                                                                                                                                                                                                                               Score 34; DB 6;
Pred. No. 1.9e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 13;
Pred. No. 1.9e+02;
Mismatches 0;
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E6FB221909BFD20B CRC64;
                                                                                                                                                                                                                                                                                                       6A7F35C35C45EED8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta2a, and alpha2/delta subunits channels similar to those found in
                                        2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel
                                        ζ
                                                                                                                                                                                                                             .9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-type Ca2+ Channel
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                              Length 2331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                              0
                                                                                                                                                                                                              Gaps
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Search completed: March 18, 2002, 09:51:54 Job time: 283 sec
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RETISSUE-DORSAL ROOT GANGLION NEURONS;

RAL LU O., Dunlap K.;

RT "Cloning and Functional Expression of Novel N-type Ca2+ Channel Type Lu J. Biol. Chem. 0:0-0(1999).

REMBL; AF173018; AAD51821.1;

REMBL; AF173018; AAD51821.1;

REMBL; AF173018; AAD51821.1;

REMBL; AF173018; AAD51821.1;

RINterPro; IPR000636; Catton_chan_non_lig.

InterPro; IPR001682; Channel_pore_Ca_Na.

InterPro; IPR001596; Na_channel.

RINTERPRO; IPR002077; Ca_channel.

RINTERPRO; IPR002211; Cat_channel_TrpL.

PRINTS; PR00170; NACHANNEL.

DR PRINTS; PR00170; NACHANNEL.

DR PRINTS; PR00170; NACHANNEL.

SQ SEQUENCE 2332 AA; 264176 MM; ECB13B79544F0594 CRC64;
                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 34; DB 13; Length 2332; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                          1 RHRGGS 6
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958 RHRGGS 963
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
N-TYPE CALCIUM CHANNEL ALPHA-1B CDB7 VARIANT.
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Title:
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Sequence:
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AAU04932	AAU04931	AAU04930	AAW26725	AAW26724	AAW26723	AAW26722	AAR11756	AAR23813	AAR23812	AAU04929	AAU04928	AAU04927	AAU04921	AAU04920	AAU04919	AAU04918	AAW26721	AAW26720	AAW26719	AAW26713	AAW26712	AAW26711	AAW26710	AAR07246	AAR07245	AAB92200	AAY42738	AAB90794	AAU04913	AAW31587	AAR07986	AAP81179	AAP82007
Human Plasminogen	Human Plasminogen	Human Plasminogen	PAI-1 mutant V343A		1 muta	PAI-1 mutant R346A	Human PAI-1 P1-P1'	l (Arg	•	Human Plasminogen	Human Plasminogen.	Human Plasminogen	Human Plasminogen		Human Plasminogen	Human Plasminogen				Plasminogen activa		act	۲	PAI-1(E351->R). H	PAI-1(E350->R). H	Ē	alpha-		_	Human plasminogen	3	ence of human	Beta plasminogen a

ALIGNMENTS

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Lawrence DA, Stefansson SP;	(AMNA-) AMERICAN NAT RED CROSS.	12-APR-1996; 96US-0015299.	11-APR-1997; 97WO-US06071.		W09/39028-A1.		Synthetic.	Homo sapiens.		thrombosis; anglogenesis; therapy.	neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;	periodontal disease; arthritis; HIV; atherosclerosis; restenosis;	cystic fibrosis; atopic dermatitis; pancreatitis;	acute lung inflammation; alpha l-antitrypsin deficiency;	cell proliferation; emphysema; adult respiratory distress syndrome;	elastase; inhibitor; vitronectin; cell attachment; cell migration;	Plasminogen activator inhibitor type 1; PAI-1; human;		and the second of the second o

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC human plasminogen activator inhibitor (PAI) mature protein (see Luman plasminogen activator inhibitor (PAI) mature protein (see CC also AAW31587). It has an Ala for Val substitution at amino acid cresidue 343, i.e. in the reactive centre loop of the protein of the mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAW379703) and expression in a host cell. Claimed PAI-1 mutants (see AAW379703) and expression in a host cell. Claimed PAI-1 mutants (see AAW379703) and expression in a host cell. Claimed PAI-1 mutants (see AAW379703) and expression in a host cell. Claimed PAI-1 mutants (comparison per pair of His-150, Thr-154, Leu-319 and Ide-314, and one or more of Axg-333, Axg-335, Cly-331, Ile-372 and Leu-91. The mutants are characterised by being resistant to inactivation by elastase, and by having a high affinity comparison one and and a stronger activator, plasmin, cathepsin G, chymase, gelatinases A and B, strongelysin and collagenase, and by having a high affinity cathepsin G, chymase, gelatinases A and B, strongelysin and collagenase, and by having a high affinity cathepsis (all transportation (Vn) and are used, in vivo or in vitro, to inhibit cather and the comparison of protein and collagenase, and by having a high affinity cathepsis at cather and collagenase, arthiftis and HI infection). They also inhibit Vn-stimulated cell attachment, migration and/or chapsis of the lump, wound cather and solve trauma, vascular graft restenosis, fibrosis (associated with cather and collagenase) and fibrosis grantina formation and or healtion involving and fibrosis grantination of primary condition involving apathological angiogenesis (all claimed). Since the mutants are resistant to claevage by the proteases to which they are more effective therapeutic agents. They also promote uptake and clearance of elastase (or its complex with PAI-1) condition.
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Best Local Similarity
Matches 11; Conser
            Plasminogen activator inhibitor type 1; PAI-1; human; elastase; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HTV; atherosclerosis; restenosis; periodontal disease; arthritis; HTV; atherosclerosis; psoriasis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
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                                                                                                                                                                                                  Plasminogen
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                                                                                                                                                                                                                                                                                                                                   AAW26715 standard;
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                                                                                                                                                                                               activator inhibitor mutant P4Asp (V343D).
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                                                                                                                                                                                                                                                                                                                                   Protein;
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RESULT AAW26716

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Matches Query Match Best Local S

Similarity

100 0;

Score 55; .DB 18; Pred. No. 0.022; 0; Mismatches 0;

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Length 379;

Conservative

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CC human plasminogen activator inhibitor (PAI-1) mature protein (see also AAMA31587). It has an Asp for Val substitution at amino acid calso AAMA31587). It has an Asp for Val substitution at amino acid comparative and the protein activator in the reactive centre loop of the protein. The commutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAM797303) and expression in a host cell. Claimed PAI-1 mutants (see AAM26710-25) have at least one amino acid substitution at amino acid substitution at composition 343-350, especially at position 343 and/or 346, and may be expression in a host cell. Claimed PAI-1 mutants (see AAM26710-25) have at least one amino acid substitution at position of His-150, Thr-154, Leu-319 and Ide-354, and one or more of four of His-150, Thr-154, Leu-319 and Ide-354, and one or more of Arg-333, Arg-335, Gly-331, Ide-372 and Leu-91. The mutants are characterised by being resistant to inactivation by elastase, plasminogen activator, plasmin, cathepsin (s. chymase, gelatinases A composition of plasminogen activation (specifically in emphysema, adult respiratory distress syndrome, acute lung inflammation, congenital alpha 1-antitypsin deficiency, cystic fibrosis, atopic dermatitis, capanteratitis, periodontal disease, arthritis and HIV infection).

CC post-angioplasty restencesis, neointima formation after vascular migration induced proliferation (specifically in atherosclerosis, cost-fically in 
                                                                                                 promote uptake and clearance of elastase (or its complex with PAI-1) by receptors.

(NB. the amino acid sequence of the mutant protein was obtained by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
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Synthetic.
Sequence
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                                                                      (NB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMNA-) AMERICAN NAT RED CROSS
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     Ä,
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inclair Cain be obtained by streetching the contract call. Claimed pAt-1 mutants it (see AAW26710-25) and expression in a host cell. Claimed pAt-1 mutants it position 343-350, especially at position acid substitution at position 343-350, especially at position acid substitution at position 343-350, especially at position 343-360/07-346, and may it position 343-350, especially at position 343-360/07-346, and may it is comprising between one and it is comparable to the comparable of the comparab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises a preferred mutant, P4Gly (V343G), of human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has a Gly for Val substitution at amino acid residue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAM37303) and expression in a host cell. Claimed PAI-1 mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasminogen activator inhibitor type 1; PAI-1; human; elastase; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HTV; atherosclerosis; restenosis; neolntima; fibrosis; wound healing; tumour; metastasis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                             promote uptake and clearance of elastase (or its
(NB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy
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                                                                                complex with PAI-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or
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AAW26717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
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This polypeptide comprises a preferred mutant, P4Leu (V343L), of human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has a Leu for Val substitution at amino acid cresidue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAW36710-25) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may have additional stabilising mutations comprising between one and cour of His-150, Thr-154, Leu-319 and Leu-91. The mutants are characterised by being resistant to inactivation by elastase, plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A and B, stromelysin and collagenase, and by having a high affinity pathological elastase activity (specifically in emphysema, adult respiratory distress syndrome, acute lung inflammation, congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elastase;
cell proli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen activator inhibitor mutant P4Leu (V343L).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-526399/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   periodontal disease; arthritis; HIV;
neointima; fibrosis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cystic fibrosis; atopic dermatitis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation; emphysema; adult respiratory distress syndrome;
acute lung inflammation; alpha 1-antitrypsin deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMNA~) AMERICAN NAT RED CROSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 rmapeeiimdr 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RMAPEEIIMDR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page -; 144pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          en activator inhibitor type 1; PAI-1; inhibitor; vitronectin; cell attachmo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379
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milarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stefansson
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Pred. No. 0.022;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell attachment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell migration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psortasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW26718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, pariodontal disease, arthritis and HIV infection). They also inhibit Vn-stimulated cell attachment, migration and/or They also inhibit Vn-stimulated cell attachment, migration and/or constraint of the cell of trauma, vascular yraft restenosis, nebintima formation after vascular trauma, vascular graft restenosis, fibrosis (associated with chronic inflammation or chemotherapy, or of the lung), wound healing with scarring and fibrosis, growth/invasion of primary tumours or metastases, psoriasis, deep vein thrombosis and any condition involving pathological angiogenesis (all claimed). Since the mutants are resistant to cleavage by the proteases to which they bind, they are more effective therapeutic agents. They also promote uptake and clearance of elastase (or its complex with PAI-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasminogen activator inhibitor type 1; PAI-1; human; elastase; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency;
                                Claim 4; Page -; 144pp; English.
                                                               Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
This polypeptide comprises a preferred
                                                                                                                                                                 Lawrence
                                                                                                                                                                                                                                12-APR-1996;
                                                                                                                                                                                                                                                               11-APR-1997;
                                                                                                                                                                                                                                                                                                                             WO9739028-A1
                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasminogen activator inhibitor mutant P4Ile (V343I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW26718 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NB. the amino acid sequence adaptation of the wild-type s specification).
                                                                                                                                                                                              (AMNA-) AMERICAN NAT RED CROSS.
                                                                                                                                                                                                                                                                                              23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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11; Conserv
                                                                                                                                                               DA,
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                                                                                                                                                                                                                                                                                                                                                                                                           anglogenesis;
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                               Stefansson SP;
                                                                                                                                                                                                                                96US-0015299.
                                                                                                                                                                                                                                                               97WO-US06071.
                                                                                                                                                                                                                                                                                                                                                                                                            therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e of the mutant protein was obtained by sequence provided in Fig 4A of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB
Pred. No. 0.0
0; Mismatches
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 mutant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 379; 0.022;
P4Ile (V343I),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complex with PAI-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                 Synthetic.
Homo sapie
                  31-MAY-2001
                                                                                                                                 Key
Region
                                                                                                                                                                                                                                                                                      Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Ala; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome ARDS; HIV infection, Human immunodeficiency virus; prostate cancer; TRI-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                             Human Plasminogen activator inhibitor-1, PAI-1, mutant P4Ala
                                                             WO200138560-A2
                                                                                                                                                                                                                                                                          V343A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU04922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04922 standard; Protein; 379 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by receptors.
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                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                         Location/Qualifiers
332.351
/label- Reactive_centre_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                                                                                                                             syndrome;
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RESULT AAUU4923
ID AAUU4923
ID AAUU
XX AUU
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DT 26-5
XX Huma
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CC wote: The present sequence is not shown in the specification but is considered from the mature PAI-1 sequence shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 11
                                                                                              Key
Region
                                                                                                                                                                                                                                                                                                                       Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Asp; Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Asp; Humobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; ARDS; HIV infection; Human immunodeficiency virus; prostate cancer; PAI-1 mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilised on a solid substrate -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Plasminogen activator inhibitor-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU04923;
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   WO200138560-A2
                                                                                                                                                                                                                                       Synthetic
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11; Conserv
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Conservative
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                                                                                                 Location/Qualifiers 332..351
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Pred. No. 0.022;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAI-1, mutant P4Asp.
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RESULT
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CC derived from the mature PAI-1 sequence shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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                                                                                                                     Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Gly; Immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; immobilised enzyme; cystic fibrosis; acute respiratory cancer; ARDS; HIV infection; Human immunodeficiency virus; prostate cancer; TNF-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilised on a substrate -
                                                                                                                                                                                                         Human Plasminogen activator inhibitor-1, PAI-1, mutant P4Gly.
                                                                                                                                                                                                                                                                                                                 AAU04924 standard; Protein; 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Key Region

Location/Qualifiers 332..351

Homo sapiens Synthetic

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AAU04925

ID AAUC
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AC AAUC
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POT 26-5
POT 26-5
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Huma
KW Huma
KW Huma
KW ARDOS
KW TNRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents human plasminogen activator inhibitor-1, parish, mutant p401y (V3430). PAI-1 is a serine proteinase inhibitor or serpin. The protein is used to demonstrate the method of the invention which comprises detecting a functionally active form of an enzyme in a biological sample by contacting an enzyme inhibitor immobilised on a contact of the enzyme inhibitor to the active form of the enzyme the binding of the enzyme inhibitor to the active form of the enzyme by a detectable label, where the enzyme inhibitor specifically forms a covalent bond or binds, with a dissociation constant of 1 x 10-9M or less with the active form of the enzyme. The present invention provides a sensitive method for the detection of a functionally active form of an enzyme in a biological sample. Human PAI-1 can be used to detect a number of enzymes including tissue plasminogen activator, urckinase, thrombin, plasmin, neutrophil celastase, pancreatic elastase, trypsin, chymotrypsin, cathepsin, G and prostate specific antigen and as such can be used in methods to diagnose diseases such as cystic fibrosis, acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated inflammation, prostate cancer and benign prostatic hypertroph—mediated inflammation, prostate cancer and derived from the mature PAI-1 sequence shown in the specification but is
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                      Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Leu; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; tamobilised enzyme; cystic fibrosis; acute respiratory cancer; ARDS; HIV infection; Human immunodeficiency virus; prostate cancer; TNF-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page - ; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilised on a solid
               Synthetic
                                                    ARDS; HIV in:
TNF-mediated
                                                                                                                              Human Plasminogen
                                                                                                                                                         26-SEP-2001
                                                                                                                                                                                    AAU04925;
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                                                                                                                            activator inhibitor-1, PAI-1,
                                                                                                                                                                                                               Protein; 379 AA
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Pred. No.
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Best Local Similarity 100
Matches 11; Conservative
           Human; Plasminogen activator inhibitor-1; PAI-1; serpin; P4Ile; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; thmobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; ARDS; HIV infection; Human immunodeficiency virus; prostate cancer; TNF-mediated inflammation; benign prostatic hypertrophy; mutant; mutein;
                                                                                                               26-SEP-2001
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                                                                                 Human Plasminogen activator inhibitor-1, PAI-1, mutant P4Ile.
                                                                                                                                           AAU04926;
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100.0%;

Score 55; Pred. No.

DВ .022; 22;

Length 379;

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Mismatches 0

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The sequence represents human plasminogen activator inhibitor-1, corrections of the invention of the invention of reprintant P4Leu (Y343L). PAI-1 is a serine proteinase inhibitor or serpin. The protein is used to demonstrate the method of the invention which comprises detecting a functionally active form of an enzyme in a considerable by contacting an enzyme inhibitor immobilised on a considerable by contacting an enzyme inhibitor immobilised on a considerable of the enzyme inhibitor to the active form of the enzyme by a detectable the enzyme inhibitor to the active form of the enzyme in the binding of the enzyme inhibitor specifically forms a covalent bond or binds with a dissociation constant of 1 x 10-9m or less with the active form of the enzyme. The present invention provides a sensitive method for the detection of a functionally active form of an enzyme in a biological sample. Human pAI-1 can be used to detect a number of enzymes including tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil constate specific antigen and as such can be used in methods to diagnose (ARDS), HIV infection, TNF-mediated inflammation, prostate cancer and consign prostatic hypertrophy.

Note: The present sequence is not shown in the specification but is
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Region
                                           derived from the mature PAI-1 sequence פּ
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379 AA;
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                                                                       sequence shown
                                                                   in the specification but shown in figure 5.
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AAR08411
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Best Local Similarity
Matches 11; Conserv
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Region
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                                          Plasminogen Activator Inhibitor; fibrinolysis; liver transplants.
                                                                                                                              Modified mature Plasminogen Activator Inhibitor PAI-1.
                                                                                                                                                                                                                                   27-FEB-1991
                                                                                                                                                                                                                                                                                                                            AAR08411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ARDS), HIV infection, TNP-mediated inflammation, prostate cancer and benign prostatic hypertrophy.

Note: The present sequence is not shown in the specification but is derived from the mature PAI-1 sequence shown in figure 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMNA-) AMERICAN NAT RED CROSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RMAPEEIIMDR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atch 100.0%; cal Similarity 100.0%; 11; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 AA;
                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9905-0167553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 22;
Pred. No. 0.022;
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Query Match
Best Local S
Matches 11
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See also AAQ06590-Q06594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The N-terminal sequence of this protein can be deleted to leave SIVH or VH. The Val residue of mature PAI-1 corresponds to residue 24 of the preprotein. It may alternatively begin MVH. The protein is used in tests to identify inhibitors of its binding to tissue plasminogen activator. It is also used therapeutically to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant functional human plasminogen activator inhibitor - and plasmid expression vectors for its prodn. in E. coli, used for assays of T-PA PAI-1 inhibitors and treatment of excessive fibrinolysis
25-FEB-1988
                             W08801273-A
                                                                        Modified-site
                                                                                                    Modified-site
                                                                                                                                 Modified-site
                                                                                                                                                            Protein
                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                             Endothelial plasminogen activator inhibitor
                                                                                                                                                                                                                                                                                         Beta plasminogen activator inhibitor encoded
                                                                                                                                                                                                                                                                                                                      16-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                   AAP82007;
                                                                                                                                                                                                                                                                                                                                                                               AAP82007 standard; protein; 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 30; Page 43; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA;
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                                                                          label-putative glycosylation site
329..331
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                    label-putative glycosylation site
                                                                                                                                           abel- mat_beta-PAI
                                                                                                                                                                        label-signal sequence
                                                          abel-putative glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 11; Length 382; 100.0%; Pred. No. 0.023; rative 0; Mismatches 0; Indels
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RESULT
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The lambda 3 clone DNA or plasmid pPAI3 can be used to produce the inhibitor by recombinant DNA technology. The protein inhibits both t-pA and u-pA and is immunologically different from protease nexin and placental PAI. It can also be used in a solid phase assay for detection of endothelial PAI, and as an immunogen to raise antibodic for use as receptor molecules in other assay systems. See also AAP80252-54.
                                                                                                                                                                                                                                                                                                                                      Sequence of human endothelial encoded by PAI2350 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnostic assays for tissue - and urokinase-type plasminogen inhibitor - and pure, recombinant human endothelial plasminogen activator inhibitor.
Disclosure; ; p;
                                       Recombinant DNA coding human endothelial plasminogen activator inhibitor used for obtaining prods. having effect on blood coagulation or
                                                                               WPI; 1988-079089/12.
N-PSDB; AAN81524.
                                                                                                                                                                           12-SEP-1986;
                                                                                                                                                                                                      11-SEP-1987;
                                                                                                                                                                                                                                23-MAR-1988
                                                                                                                                                                                                                                                         EP260757-A.
                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                              Protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                        AAP81179;
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                                                                                                                                                (STCL ) STICHT INSTAND BLOEDTRAN.
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                            fibrinolysis
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DB; AAN80253.
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Similarity 100.
11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 AA;
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                                                                                                                                                                           86NL-0002307
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 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sawdey M;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                    plasminogen activator inhibitor (PAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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0.023;
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RESULT
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Matches 11
A human umbilical cord endothelial cell cDNA library was screened with 4 oligonucleotide probes based on the Known PAI-1 sequence. A 2.1kb insert was identified in the most strongly positive clones. It was inserted into pTZ19R to give pECB3-1 and the sequence given here. To produce mature protein, the leader sequence was removed by partial digestion with ApaLI and NS1I of HaeIII-methylase treated pECB3-1 DNA. The resulting 1800bp fragment was attached to an adaptor (to restore the first 2, Met-Val, amino acids), digested with Ncol and inserted onto Ncol-PStI cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colonies of human endothelial cDNA were screened using the probe (AANRI522) and a heterologous antiserum to detect the presence of human endothelial PAI like polypeptides. Novel recombinant DNA molecule for use in cloning and/or expressing DNA sequence in host cells which contains, in addition to a vector protein, a DNA sequence coding for human PAI is
                                                                                                                              Disclosure; Page 8; 49pp; English.
                                                                                                                                                                  New recombinant functional human plasminogen activator inhibitor and plasmid expression vectors for its prodn. in E. coli, used for assays of T-PA PAI-1 inhibitors and treatment of excessive
                                                                                                                                                                                                                                                          Davis GL, Knabb RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                        WPI:
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                                                                                                                                                                                                                                                                                                                                       08-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                         W09013648-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                        fibrinolysis
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DB; AAQ06594.
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11; Conserv
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                                                                                                                                                                                                                                                                                    PONT DE NEMOURS CO.
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nilarity 100.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activator Inhibitor PAI-1 encoded by clone ECE3-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                              89US-0350264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  /label= mature PAI-1
/note= "Met residue present as
PAI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitor;
                                                                                                                                                                                                                                                            Reilly TM,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibrinolysis;
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0.024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver transplants
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AAW31587
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Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elastase inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha l-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neolntima; fibrosis; wound healing; tumour; metastasis; psoriasis; thrombosis; angiogenesis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pKK233-2 to give plasmid ptAC-PAI. This expresses mature PAI-1 with the N-terminus Val-His-His which is useful in tests to identify inhibitors of its binding to tisse plasminogen activator. The protein is also used therapeutically to treat excessive or inappropriate fibrinolysis, e.g. during liver transplant surgery. See also AAQ06590-Q06593.
                                                                                                                                                                                                                                                                                                                                                    /note-
Misc-difference 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW31587;
                                                                                                                                                                                                                                                                                                                  Misc-difference 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasminogen activator inhibitor type 1; PAI-1; human;
elastase inhibitor; vitronectin; cell attachment; cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW31587 standard; Protein; 402 AA
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23-OCT-1997.
                                                                                           Misc-difference
                                                                                                                                                            Misc-difference 369
                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human plasminogen activator inhibitor type 1.
                              W09739028-A1
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ilarity 100.0%;
Conservative 0
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                                                                                                                        /label- P1
/note- pre
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                                                                                                                                                                                                                                                                       342
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Sig_peptide 24..402
                                                                                                                                                                     /label= P4
/note= "preferred substitution site
elastase inhibitor mutant"
                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Mat_protein
/note= "Claim 3"
                                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                      /note-
                                                            "preferred substitution site substitution"
                                                                                                           "preferred substitution site elastase inhibitor mutant"
                                                                                                                                                                                                                                       "preferred substitution site stabilisation"
                                                                                                                                                                                                                                                                                      "preferred substitution site stabilisation"
                                                                                                                                                                                                                                                                                                                                    "preferred subsitution site for
stabilisation"
                                                                                                                                                                                                                                                                                                                                                                                     "reactive centre loop region"
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Pred. No. 0.024;
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Search completed: March 18, 2002, 09:48:55 Job time: 364 sec

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Best Local S
Matches 11
                                                                                                                                                                 This polypeptide sequence comprises wild-type human plasminogen activator inhibitor type (PAI-1). Novel mutants (see AM26710-25) c the PAI-1 mature protein are claimed that inhibit elastase or other elastase-like proteases, or are inhibitors of vitronectin-dependent cell migration. The mutants are obtained by site-directed mutagenesis of the PAI-1 DNA sequence (see AAT97303) and expression in host cells, and have a range of therapeutic uses. Preferred mutants have amino acid substitutions in the reactive centre loop region (especially at position 343 and/or 346 of the mature protein), and may have additional stabilising amino acid substitutions at 1-4 of residues 130, 154, 319 and 354, and 1-5 of residues 333, 335, 331, 372 and 91.
                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 4A; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1997;
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence DA,
369 rmapeelimdr 379
               1 RMAPEEIIMDR 11
                                                 AMERICAN NAT RED CROSS.
                                                                                                                                       402 AA;
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                                                                                           DB 18; Length 402;
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Title: Perfect score: Sequence:

US-09-544-665-2 55 1 RMAPEEIIMDR 11

RMAPEEIIMDR 11

Run on: OM protein -

protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Minimum DB Maximum DB

seq

length: 0 length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA: *

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of hits satisfying chosen parameters:

212252 seqs, 22503292 residues

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March 18, 2002, 09:49:40; Search time 37.77 Seconds (without alignments) 6.554 Million cell updates/sec
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                                                                                               TOPOLOGY: US-08-840-204-3
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US-08-840-204-3
                                         Query Match
Best Local S
Matches 11
                                                                                                              TELEPHONE: (202) 887-1500
TELEPAX: (202) 822-0168
TELEFAX: (202) 822-0168
TELEY 90-4030 MESNFORENSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application Patent No. 6103498 GENERAL INFORMATION:
                                                                                                                                                                                         COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, v
REPAIRING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204
FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30807-200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRHUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
 346 RMAPEEIIMDR 356
                                                                                                                                                                                                                                                                                                                                                                               STREET: 2000 PENICITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
            1 RMAPEEIIMDR 11
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5, 6103498
                                         1 Similarity 100.
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US-09-232-190-63
US-09-232-197-63
US-08-677-049-5
US-08-959-011-3
US-09-232-191-9
US-09-232-197-95
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US-09-232-200-71
US-09-232-197-42
US-09-232-197-42
US-09-232-197-42
US-09-232-197-71
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                                                      Score 55; DB 3;
Pred. No. 0.008;
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                                           Mismatches
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                                           Indels
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3, Appli
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95, Appli
95, Appli
97, Appli
45, Appli
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Result No.

Match query

Length

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Description

100.0 100.0 100.

379 390 390 390 390 402 402 402 402 33 33 33 33 37 37 37 37 37 37 37 37

Sequence

444606647

pred. No. is t score greater is

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES

225 Franklin Street

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JS-08-477-108A-6
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Best Local Similarity
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                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/938
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5* DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        369 RMAPEELIMDR 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                       1 RMAPEEIIMDR 11
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                                             LE OF INVENTION: MASPIN, A NOVEL SERPIN WITH LE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6, Application US/08121714
o. 5470970
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                                                                                                                                                     6, Application US/08477108A
5. 5801001
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                                                                                                                                                                                                                                                                                                                           Conservative
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WordPerfect (Version 5.1)
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                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Fish & Richardson P.C
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                                                                                                                                                                                                                                                                                                                                          Score 55; DB 1;
Pred. No. 0.0083;
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                       08-477-112-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
MEDIUM TYPE: 3.5" D
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: L. Boston
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                               369 RMAPEETIMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                                                                                                                            PPLICANT: Sager, Ruth
ITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
ITLE OF INVENTION: TUNOR SUPPRESSING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELECOMMUNICATION INFORMATION:
           MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100
mes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 06:
LECOMMUNICATION TIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/477,108A FILING DATE: June 7, 1995 CLASSIFICATION: 536
                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/938.823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844.296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
ETITIC CATTON NUMBER: 07/662,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RMAPEEIIMDR 11
                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                       OUNTRY:
                                                                                                                                                       Boston
                                                                                                       02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                       Massachusetts
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225 Franklin Street
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50z or 55sx
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RESULT 5
PCT-US93-08322-6
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,82:
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,29)
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,21:
APPLICATION NUMBER: 07/662,21:
APPLICATION NUMBER: 07/662,21:
APPLICATION NUMBER: 03/819
ATTORNEY,AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REGERENCE/DOCKET NUMBER: 0657
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
ATTORNEY/ACENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/072001
TELECOMPUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 RMAPEEIIMDR 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US93/08322
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RMAPEEIIMDR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                       TRY: U.S.A.
02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application PC/TUS9308322
                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sager, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (617) 542-8906
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Pred. No. 0.0083;
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                                                                                              ; TOPOLOGY: 11; MOLECULE TYPE: US-08-315-461-7
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                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315.461
EILING DATE:
CONCURRENT CONCURRENT
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                             Matches
                                        Query Match
Best Local Similarity
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Best Local Similarity 100
Matches 11; Conservative
                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Peptide Mediated Enhancement Of TITLE OF INVENTION: Thrombolysis: Methods and Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 RMAPEETIMDR 379
                                                                                                                           TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY
                                                                                                                                                                                                                                                NAME: Parker, David L.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Houston
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 1 RMAPEEIIMDR 11
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Shore, Joseph D.
                             Conservative
                                                                                                                        ss: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arnold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aniel T. Eitzman
                                                                                                            protein
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                                        100.0%;
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Pred. No.
                                        Score 55; DB 1;
Pred. No. 0.0085;
                             Mismatches
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                                                       Length 402;
                             Indels
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                                                                                                                                                                                                                                                    US-08-840-204-2
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                Sequence 2, Application US/08840204 Patent No. 6103498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-948-997-4
                                                                                                                                                                                                GENERAL INFORMATION:
  STREET: ZUVV . _
STREET: ZUVV . _
CITY: WASHINGTON
STATE: DC
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                    NUMBER OF SEQUENCES:
                                                                                                                     APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
APPLICANT: STEFANSSON, STEINGRIMUR P.
APPLICANT: STEFANSON, STEINGRIMUR P.
APPLICANTION: TYPE 1 (PAI-1) AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR UMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                       369 RMAPEEIIMDR 379
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FILING DATE: Oct-10-97
CLASSIFICATION: 435
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ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           1 RMAPEEIIMDR 11
                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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COLEMAN, TIM
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 3; Length 402; ilarity 100.0%; Pred. No. 0.0085; Conservative 0; Mismatches 0; Indels
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                                                                    MORRISON & FOERSER
                                                  PENNSYLVANIA AVENUE, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309-8512
ID NO: 4:
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RESULT 10
US-09-026-408-3
; Sequence 3, Application US/09026408
; Patent No. 6303338
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; LENGTH: 402
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-348-817A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Sin
Matches 11;
                                                                 Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                         PRIOR FILING DATE: 1996
NUMBER OF SEQ ID NOS: 1'
SOFTWARE: PatentIn Ver
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09348817A Patent No. 6191260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·09-348-817A-4
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TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHWDEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 3080
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 05/:
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/348,817A CURRENT FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1997-
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               ILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20006-1812
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                TLE OF INVENTION:
369 RMAPEEIIMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 RMAPEEIIMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFMEDER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                  1 RMAPEETIMDR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RMAPEEIIMDR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H: 402 amino acids
amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                            Hastings et al.
/ENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                   PF336D1
                                                                                                                                                                                                                                                                           1996-10-11
                                                                                                                                                                                                                                                                                                                                                                                                  Activator
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100.0%; Pred. No. 0.0085;
tive 0; Mismatches 0
                                                                       100.0%; Score 55; D:
100.0%; Pred. No. 0.
tive 0; Mismatches
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                                                                                                       Length 402;
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-09-026-408-3
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Best Local Similarity 100.0%; Pred. No. 0
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08781020 Patent No. 5792749
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-75.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO: 3:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS, WHITHAM & MCGINN
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-371-2600
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                        369 RMAPEEIIMDR 379
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CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
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                                                        COUNTRY: (
ZIP: 20191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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LE OF INVENTION: M
                                                                                         Reston
: VA
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; MOLECULE TYPE: Peptide US-08-781-020-6
                                                                                                            RESULT 13
US-08-041-774-3
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; ORGANISM: Homo sapiens
US-09-038-935-6
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin
SEQ ID NO 6
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.9%; Score 50; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0
Sequence 3, Application US/08041774
Patent No. 5550114
GENERAL INFORMATION:
APPLICANT: Strayer, David S.
TITLE OF INVENTION: EPIDERMAL GI
NUMBER OF SEQUENCES: 5
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Best Local S
                                                                                                                                                                                                                                                     Matches
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CURRENT FILING DATE: 1998-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-038-935-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1997-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Janciauskiene, Sabina
Title OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW DENSITY
TITLE OF INVENTION: LIPOPROTEIN CHOLESTEROL
FILE REFERENCE: 294022ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
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TELEPHONE: 703-391-2510
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ATTORNEY/AGENT INFORMATION:
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SOFTWARE: PatentIn Release $1.0, Version $1.30
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5. 6150332
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                       David S. EPIDERMAL GROWTH FACTOR INHIBITOR
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                                                                                                                                                                                                                                                                       90.9%; Score 50; 100.0%; Pred. No.
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; MOLECULE TYPE: Protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: internal
US-08-041-774-3
                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: An epidermal
; OTHER INFORMATION: growth factor inhibitor peptide
US-08-530-340-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.0
Conservative
                                                Query Match 61.8
Best Local Similarity 55.8
Matches 5; Conservative
                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2 LENGTH: 37
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
STYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/530,340A CURRENT FILING DATE: 1995-12-22 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                       equence 2, Application US/08530340A
                                                                                                                                                                                                                                                                                                                                                                                                                      08-530-340-2
                                                                                                                                                                                                               LENGTH: 37
TYPE: PRT
                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                          PPLICANT: Strayer, David S
ITLE OF INVENTION: Epidermal Growth Factor Inhibitor
ILE REFERENCE: JEFF-0226
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 19930402
CLASSIFICATION: 514
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ZIP: 10112
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
2 MAPEEIIMD 10
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REFERENCE/DOCKET NUMBER: 2560/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
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977-9809
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Pred. No. 5.2;
3; Mismatches
                                              Score 34; DB 4;
Pred. No. 5.2;
3; Mismatches
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Search completed: March 18, 2002, 09:49:40 Job time: 224 sec
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; FRAGMENT TYPE:
US-08-041-774-5
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                                                                                                                                             Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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Patent No. 5550114
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                   MOLECULE TYPE: |
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Zivin, No. 5550114man H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                 182 LAPPEVVMD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Zivin, NO. 5550110
REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 LAPPEVVMD 24
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                                                                                                                                                                 61.8%;
55.6%;
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T35375	T38078	B83293	F64486	S47087	T19236	H75381	A70545	A49166	T37626	S61619	A75253	T08226
probable membrane probable protein	hypothetical prote	cystathionine beta		pir7b protein -	hypothetical prot	DNA-binding respon	hypothetical prote	3',5'-cyclic-AMP	DNA mismatch repa	STU2 protein - yea	glutaminyl-tRNA sy	hypothetical prot

ALIGNMENTS

plasminogen activator inhibitor type 1 precursor - American mink C:Species: Mustela vison (American mink) C:Species: Mustela vison (American mink) C:Date: 19-0ct-1995 #sequence_revision 08-Feb-1996 #text_change 20-Jun-2000 C:Accession: JC4265 R:Chuang, T.H.; Hamilton, R.T.; Nilsen-Hamilton, M. Gene 162, 303-308, 1995 Gene 162, 303-308, 1995 A:Title: Cloning of the mink plasminogen activator inhibitor type-1 messenger RNA: An A:Accession: JC4265; MUID:96032362

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plasminogen activator inhibitor 1 precursor [validated] - human N.Alternate names: plasminogen activator inhibitor, endothelial C;Species: Homo sapiens (man) C;Pate: 31 Mar 1988 #sequence_revision 31 Mar 1988 #text_change 08 Dec-2000 C;Pate: 31 Mar 1988 #sequence_revision 31 Mar 1988 #text_change 08 Dec-2000; A25895; C;Accession: A28107; S02551; A25996; I59126; J30397; A25893; A254646; A29100; A25895; C;Accession: A28107; S02551; A25996; I59126; J30397; A25893; A26146; A29100; A25895; R;Bosmac, P.J.; Van den Berg, E.A.; Koolstra, T.; Slemieniak, D.R.; Slightom, J.L. J. Biol. Chem. 263, 9129-9141, 1988
J. Title: Human plasminogen activator inhibitor-1 gene. Promoter and structural gene names activator activator inhibitor-1 gene. Promoter and structural gene names activator activator inhibitor-1 gene. Promoter and structural gene names activator activator inhibitor-1 gene. Promoter and Structural gene names activator activat
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C;Superfamily: antithrombin III
C;Superfamily: antithrombin III
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasminogen activator; serine proteinase inhibitor
E;1-21/Domain: signal sequence #status predicted <SIG>
E;1-21/Domain: signal sequence #status predicted <NAT>
F;22-400/Product: plasminogen activator inhibitor type 1 #status predicted <NAT>
F;23-20,286,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;367/Inhibitory site: Arg (plasminogen activator) #status predicted
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A;Residues: 1-400 <CHUO
A;Residues: 1-400 |
A;CROSS-references: EMBL:X58541; NID:gl164923; PIDN:CAA41433.1; PID:gl164924
A;Experimental source: lung CCL64 epithelial cells
C;Comment: This protein controls the activities of the plasminogen activators and
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A;Molecule type: DNA
A;Residues: 1-402 <BOS>
A;Residues: 6B:J03764; NID:g189564; PIDN:AAA60007.1; PID:g386996
A;Cross-references: GB:J03764; NID:g189564; PIDN:AAA60007.1; PID:g386996
BY:Crandberg, L.; Lawrence, D.; Ny, T.
Eur. J. Biochem. 176, 609-616, 1988
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367 RMAPEEIIMDR 377
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A; Title: Plasminogen activator inhibitor type-1: A; Reference number: A91371; MUID:87080762 A; Accession: A25651 A; Molecule type-1: A; Molecule 
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 17-402 < WUN>
A; Residues: 17-402 < WUN>
A; Residues: 17-402 < WUN>
A; Cross-references: GB: X04744; NID: g35275; PIDN: CAA28444.1; PID: g755747
A; Note: part of this sequence, including the amino end of the mature processor, and the sequence, D.; Millan, J.L.; Loskutoff, D.J.
R; Ny, T.; Sawdey, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 6776-6780, 1986
A; Title: Cloning and sequence of a cDNA coding for the human beta-migra
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A;Note: the complete translation is not annotated in GenBank entries HSPA111, HSPA112, HR;Loskutoff, D.J.; Linders, M.; Keijer, J.; Veerman, H.; van Heerikhuizen, H.; Pannekoel Biochemistry 26, 3763-3768, 1987
A;Title: Structure of the human plasminogen activator inhibitor 1 gene: nonrandom distr: A;Reference number: A26996; MUID:88000586
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FEBS Lett. 210, 11-16, 1987
A;Title: cDNA cloning and expression in E.
A;Beference number: A29100; MUID:87105925
A;Accession: A29100
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R;Ginsburg, D.; Zeheb, R.; Yang, A.Y.; Rafferty, U.M.; Andreasen, P.A.; Nielsen, J. Clin. Invest. 78, 1673-1680, 1986
R;Title: cDNA cloning of human plasminogen activator-inhibitor from endothelial clyreference number: A92766; MUID:87058123
R;Accession: A26146
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Fittle: Structure and expression of the human Reference number: JS0397; MUID:90128289
Accession: JS0397
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Residues: 20-402 <NYT>
(Cross-references: GB:M14083)
Andreasen, P.A.; Riccio, A.;
BBS Lett. 209, 213-218, 1986
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Residues: 1-9 <ZON>
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Nucleic Acids Res. 17, 8872, 1989
A;Title: cDNA for bovine type 1 p.
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A; Accession: S74133
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A;Cross-references: GB:X04729;
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A; Residues: 1-402 <MIM>
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A; Residues: 225-235 <LAU>
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Matches 11
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Accession: S06745
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              Transforming
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l1; Conservative
              growth factor-beta 1 modulates basic fibroblast growth factor-i
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K;Stroemqvist, M.; Karlsson, K.E.; Bjoerquist, P.; Andersson, J.O.; Bystroem, M.; Han Blochim. Biophys. Acta 1295, 103-109, 1996
A;Title: Characterization of the complex of plasminogen activator inhibitor type 1 wi A;Reference number: S70346; MUID:96283799
A;Status. S70346
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A;Residues: 225-235 <LAU.
A;Residues: L; Martensen, P.M.; Sottrup-Jensen, L.; Jus Bur. J. Blochem. 241, 38-46, 1996
A;Title: Conformational changes of the reactive-centre number: S74133; MUID:97054589
                                                                                                                                                                                                                                                                                                                                plasminogen activator inhibitor-1 precursor - bovine N;Alternate names: endothelial-ceel plasminogen activator inhibi C;Species: Bos primigenius taurus (cattle) C;Date: 28-Feb-1990 #sequence_revision 22-Apr-1995 #text_change C;Accession: S06745; A35855; S01324; S19906
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A; Residues: 370-375 <STO>
C; Comment: This inhibitor acts as "bait" for tissue plasminogen activator
C; Comment: This inhibitor acts as "bait" for tissue plasminogen activator
C; Comment: The et also Pai have been identified (see also PIR: A32853 ano oma cells. Vascular endothelial cells may be the primary site of synthesis
C; Comment: Glycosylation is not required for inhibitory activity.
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A;Cross-references: GDB:120297; OMIM:173360
A;Map positition: 7921.3-792
A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1; 363/1;
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A;Title: Isolation of multiple types of plasminogen activator inhibitors from vascula A;Reference number: A60436; MUID:90020174
A;Recession: A60436
A;Cross-references: EMBL:X16383; NID:9600; R;Pepper, M.S.; Bellin, D.; Montesano, R.; Coll Biol. 111, 743-755, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: glycoprotein; serine proteinase inhibitor F;1-23/Domain: signal sequence #status predicted <SIG> F;1-23/Domain: signal sequence #status predicted <SIG> F;24-402/Product: plasminogen activator inhibitor-1 #status experimental F;232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicter;369/Inhibitory site: Arg (plasminogen activator) #status predicted
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                                                                                                                                                                                                       ovine type 1 plasminogen
S06745; MUID:90067867
                                                                                                                                                                                                                                                                                                      Hattori, M.; Luskutoff,
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Pred. No. 0.0
0; Mismatches
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                                             Orci,
                                                                           PIDN:CAA34419.1;
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, B.L.; Baker,
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R:Zeheb, R.; Gelehrter T.D.
Gene 73, 459-468, 1988
A:Title: Cloning and sequencing of cDNA for
A:Reference number: JT0490; MUID:89211983
A:Accession: JT0490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasminogen activator inhibitor 1 precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Depcies: Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A35032; JT0490; A60581; A39120 R;Bruzdzinski, C.J.; Riordan-Johnson, M.; Nordby, E.C.; Suter, S.M.; Gelehrt J. Biol. Chem. 265, 2078-2085, 1990 A;Title: Isolation and characterization of the rat plasminogen activator in A;Reference number: A35032; MUID: 90130456
                                                                                                                                 A; Molecule type: protein
A; Residues: 24-48 (NEM>
A; Residues: 24-48 (NEM>
R; Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, R; Olson Jr., J.A.; Shiverick, B., 1928-1932, 1991
A; Title: Anglotensin II induces secretion of plasminogen activator inl
A; Reference number: A39120; MUID: 91156719
A; Reference number: A39120; MUID: 91156719
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A; Residues: 1-402 <ZEH>
A; Residues: 1-402 <ZEH>
A; Cross-references: GB:M24067; NID:g577500; PIDN:AAA56856.1; PID:g577501
A; Cross-references: GB:M24067; NID:g577500; PIDN:AAA56856.1; PID:g577500; PIDN:AAA56856.1; PID:g5775
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A; Residues: 24-49, 'L', 51-63 <KAT>
C; Comment: Three types of PAI have been identified. PAI-1 is an acid-stable glycoprotein
may be the primary site of synthesis of plasma PAI.
C; Comment: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, an
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R:Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.
Eur. J. Biochem. 176, 81-87, 1988
A;Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and A;Reference number: S01324; MUID:88329072
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A60581; MUID:90276328
A; Accession: A60581
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A;Accession: A35855
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Molecule type: protein Residues: 24-43,'G' <OLS>
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Residues: 153-235 <PEP>
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Pred. No. 0.0067;
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    A;Status:
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A; Residues: 1-197 <BLAT>
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A; Residues: 1-197 <LIP>
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    preliminary
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A;Gene: grpE
A;Gene: grpE
C;Superfamily: heat shock protein grpE
C-2-197/Product: heat shock protein B25.
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617
A;Recession: A65040
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C;Superfamily; antithrombin III
C;Superfamily; antithrombin III
C;Reywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-402/Product: plasminogen activator inhibitor-1 #status experimental <MAT>
F;86,232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;369/Inhibitory site: Arg (plasminogen activator) #status predicted
C;Accession: H85907
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; I iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamot Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Recession: H85907
                                                                                                                                                                                    hypothetical protein grpE [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli C;Species: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 31-Mar-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE000347; GB:U00096; NID:g2367142; PIDN:AAC75663.1; PID:g1788
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lipinska, B.; King, J.; Ang, D.; Georgopoulos, C. Nucleic Acids Res. 16, 7545-7562, 1988
A;Title: Sequence analysis and transcriptional regulation A;Reference number: S01240; MUID:88319942
A;Accession: S01240
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N;Alternate names: grpE protein

C;Species: Escherichia colli

C;Date: 28-Aug-1999 #sequence_revision 28-Aug-1989

C;Accession: S01240; A55040
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Best Local Similarity 63.0
Matches 7; Conservative
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63.6%;
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Pred. No. 1.6;
1; Mismatches
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Pred. No. 2.2;
3; Mismatches
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Burland, V.;
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protein T23G18.18 [imported] - Arabidopsis thaliana C; Speckes: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001 C; Accession: A86217 C; Accession: A86217 R; TheoLogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Authors: Hughes, B.; Huizar, L. Accession: A86217 A; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Muthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Ccession: A86141; MUID:21016719 A.; Accession: A86141; MUID:21016719
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                                                                                                  A; Status: preliminary
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C:Superfamily: heat shock protein grpE
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A;Cross-references: GB:AE005174; NID:g12517038; PIDN:AAG57724.1; GSPDB:GN00145; UWGP:Z39
A;Experimental source: strain 0157:H7, substrain EDL933
  ;Cross-references: GB:AE005172; NID:g6579201; PIDN:AAF18244.1; GSPDB:GN00141; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Molecule type: mRNA;Residues: 1-402 <PRE>;Residues: 1-402 <PRE>;Cross-references: GB:M33960; NID:g200219; PIDN:AAA39887.1; PID:g200220;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D. ur. J. Biochem. 224, 863-871, 1994 ur. J. Biochem. 224, 863-871, 1994 printle: Characterization of the murine plasma fibrinolytic system.;Reference number: S48202; MUID:95010076;Reference number: S48202; MUID:95010076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Prendergast, G.C.; Diamond, L.E.; Dahl, D.; Cole, M.D. ol. Cell. Biol. 10, 1265-1269, 1990 or The c-myc-regulated gene mrl encodes plasminogen activator inhibitor;Reference number: A34761; MUID:90158593
                                                  Molecule type: DNA
Residues: 1-382 <STO>
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Best Local
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:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Accession: A34761; 548208
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7; Conserv
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8; Conservative
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Pred. No. 1.6;
1; Mismatches
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Appl. Microbiol. Biotechnol. 38, 493-501, 1993 A;Title: Cloning and molecular analysis of the A;Reference number: A48376; MUID:93159750 A;Scatus.
                                                                                                                                                                         A;Status: preliminary
A;Molecule type: nucleic acid
A;Molecule type: cLIE>
A;Residues: 1-692 (AIE>
A;Cross-references: GB:S54369; NID:g298249; PIDN:AAC60431.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:124660,
                                                                                                                                                                                                                                                                                                                                                     orf5 3' to phbC - Thiocystis violacea
C;Species: Thiocystis violacea
C;Date: 19-Nov-1993 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: E48376
C;Accession: E48376
R;Liebergesell, M.; Steinbuchel, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: catalyzes the transfer of xylose from UDP-xylose to the C;Superfamily: Arabidopsis thaliana beta-1,2-xylosyltransferase C;Keywords: glycosyltransferase
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A;Gene: xylT
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A;Molecule type: mRNA
A;Residues: 1-534 <STR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Strasser, R.; Mucha, J.; Mach, L.; Altmann, F.; Wilson, I.B.H.; Gloessl, J.; Steinl FEBS Lett. 472, 105-108, 2000
A;Title: Molecular cloning and functional expression of beta 1,2-xylosyltransferase (A;Reference number: 226156
A;Recession: T52649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-1,2-xylosyltransferase [validated] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: T23G18.18
A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 6
                                                                                                Query Match
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                Matches
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49 RLAPEVVILD 58
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                                                                              Conservative
                                                                                             65.5%;
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                                                                         ; Score 36; DB:
; Pred. No. 60;
3; Mismatches
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Pred. No. 45;
2; Mismatches
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Pred. No.
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Mismatches
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NCBIP:124665)
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us-09-544-665-2.rpr

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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woose, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate reducing archaed A;Reference number: A69250; MUID:98049343
A;Accession: D69274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001093; GB:AE000782; NID:g2689416; PIDN:AAB91037.1; PID:g26504 C;Superfamily: probable acyl-CoA ligase medium chain; acetate--CoA ligase homology F;50-530/Domain: acetate--CoA ligase homology <ACL>
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C;Accession: D69274
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dc., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Fleischmann, R.D.; Qverbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
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Nature 390, 364-370, 1997
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec:1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA; Molecule type: DNA; Residues: 1-540 <KLE>
                                                                                                                                                                                                                                                                                                    Cross-references: SGD:S0000842; MIPS:YER040w; Map position: 5R; Superfamily: GATA-type zinc finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Sequence and expression of GLN3, Reference number: S22280; MUID:92049353; Accession: S22280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LN3 protein - yeast (Saccharomyces cerevisiae);Alternate_names: protein YER040w
                                                                                                                                                                                                                                                                                                                                                                                                                Status: not compared with conceptual translation; Molecule type: DNA; Residues: 1-473,'G',475-730 <MIN>
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ol. Cell. Biol. 11, 6216-6228, 1991
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Accession: S50543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Saccharomyces cerevisiae
|Date: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
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Best Local
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Best Local Similarity
Matches 7; Conserv
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303-355/Domain: GATA-type zinc finger homology <GZF>
306-330/Region: zinc finger GATA motif
                                                                                                                                                                                                                                                                                                                                                                           Gene: SGD:GLN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:U18796; NID:g603265; PIDN:AAB64575.1; PID:g603273; MIPS:YER040
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Residues: 1-730 <DIE>
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Description: The sequence of S. cerevisiae cosmids 9379,
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                                                                                                                          : Score 35; DB: Pred. No. 99; 1; Mismatches
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Pred. No. 71;
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A;Status: preliminary
A;Molecule type: protein
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Am. J. Pat
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DNA-directed DNA polymerase (EC 2.7.7.7) - Chlorella virus CV-NY-2A C;Species: Chlorella virus CV-NY-2A C;Date: 17-Feb-1994 #sequence_revision 17-Peb-1994 #text_change 11-C;Accession: B42543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: genomic RNA
A;Residues: 1-2095 <ACC>
A;Cross-references: EMBL:X68414; NID:g62199; PIDN:CAA48478.1; PID:g62200
C;Superfamily: Uukuniemi virus RNA-directed RNA polymerase
C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Accardi, L.; Gro, M.C.; di Bonito, P.; Giorgi, C. submitted to the EMBL Data Library, September 1992 A;Description: Toscana virus genomic L segment: molecular cloning, coding strategy a A;Reference number: S29529 A;Accession: S29529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: herpesvirus DNA-directed C; Keywords: DNA binding; DNA biosynthes; C; Keywords: DNA binding; DNA biosynthes; F; 182-199/Region: exonuclease pattern B F; 388-401/Region: exonuclease pattern C
Am. J. Pathol. 142, 1141-1153, 1993
A;Title: A 34-kd protein with strong homology
A;Reference number: A56771; MUID:93235943
A;Accession: A56771
                                                                                                                          34K epidermal growth factor inhibitor, ras-like - rabbit (fragments) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 28-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Contains: RNA-directed
C; Species: Toscana virus
C; Date: 22-Nov-1993 #sequ
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A;Title: The DNA polymerase
A;Reference number: A42543;
A;Accession: B42543
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A;Residues: 1-913 <GRA>
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Best Local S
Matches 5
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                                        n: A56771
D.S.; Mathew, J.
Chol. 142, 1141-1153, 1993
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21-731, 1992
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MUID:92263776
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4; Mismatches
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pred. No. 3.2e+02;
5; Mismatches 1
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Search completed: March 18, 2002, 09:50:30 Job time: 239 sec	OY 2 MAPERIND 10 : :: Db 27 LAPPEVVMD 35	Query Match 61.8%; Score 34; DB 2; Length 48; Best Local Similarity 55.6%; Pred. No. 7.4;. Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	A;Residues: 1-48 <str> C;Superfamily: ras transforming protein; translation elongation factor Tu homology C;Keywords: GTP binding</str>
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March 18, 2002, 09:52:24; Search time 24.53 Seconds (without alignments) 16.442 Million cell updates/sec
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   Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X58541; CAA41433.1; -.
HSSP; P01008; 1ATH.
InterPro; IPR000215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
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ACT_SITE
CARBOHYD
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SEQUENCE
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P50449;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR: PRECURSOR (PAI-1) (ENDOTHELIAL PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPIREI OR PAI OR PLANHI OR PAI-1.
Mustela vison (American mink).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIGNAL 1 21 POTENTIAL.
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SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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   100.0%; ilarity 100.0%; Conservative 0;
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429
468
492
796
7963
1373
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1373
                                                                                                                                                ME.
                                                                                                                                         POTENTIAL.

PLASMINGEN ACTIVATOR INHIBITOR-1.

REACTIVE BOND (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .) (POTENTIAL).
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URAA_ECOLI
VASI_BOVIN
VASI_BOVIN
ARKE_THEMA
YEZ9_YEAST
MSHL_YEAST
MSHL_YEAST
MPOB_RICCN
RPOB_RICCN
RPOB_RICMA

      Score 55; DB 1; 1
Pred. No. 0.0017;
); Mismatches 0;
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                                                           Length 400;
         Indels
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p33780 escherichia
p40682 bos taurus
constantus
p39454 saccharomyc
p23846 saccharomyc
p23946 thermotoga
p39398 thermotoga
p3941 rickettsia
p3741 rickettsia
p3743 rickettsia
p3744 rickettsia
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Result No.

Score

Query Match

Length

DB

ij

Description

mustela

taurus

sus scrofa

100.0

PAI1_MUSVI PAI1_BOVIN

P20961 P09372 P22777 O31066 P45365 P18494 P30320

588.22

0832125 0832125 0842558 P17080 P217080 P217080 P2180372 P38372 P38372 P466926 P466926 P466926 O13921 O13921 O13921 O14432 O540712 O540

PAII_HUMAN
PAII]_PIG
PAII_RAT
GRPE_ECOLI
PAII_RAT
GRPE_ECOLI
PAII_RAT
GRPE_CAUCR
CHVN2
GLN3_YEAST
DPOL_CHVN2
MOBE_ECOLI
RANT_MOUSE
RAN_HUMAN
MOUSE
KAD_BACHD
SYQ_DEIRA
STU2_YEAST
MSHI_SCHYON
MSH_SCHYON
PI7B_ORYSA
YE95_METJA
METC_SALTY
YD87_SCHPO
PI7B_ORYSA
METC_SALTY
CN3A_HUMAN
MCN3A_RAT
RPAII_TRYBB
KAD_ECOLI
RAD_YEREN
PKX1_HUMAN
PKX1_HUMAN

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Minimum DB Maximum DB

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length: 0 length: 2000000000

Searched:

Total number

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chosen parameters:

100059 seqs, 36664827 residues

Scoring table: Sequence: Title: Perfect score:

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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SEQUENCE OF 24-63.
SEQUENCE OF 24-63.
MEDLINE-88329072; PubMed-3262060;
Katagiri K., Okada K., Hattori H., Yano
"Bovine endothelial cell plasminogen ac
Purification and heat activation.";
""" J. Biochem. 176:81-87(1988).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-90067867; PubMed-2587231;
MEDLINE-90067867; PubMed-2587231;
MIDURO J., Savdey M., Hatiori M., Loskutoff D.J.;
MIDURO J., Savdey M., Hatiori M., Loskutoff D.J.;
"CDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).";
"CDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).";
"CDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90338128; PubMed-1696269; Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.; Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.; "Transforming growth factor-beta 1 modulates basic fibroblast growth factor-induced proteolytic and angiogenic properties of endothelial cells in vitro.";
J. Cell Biol. 111:743-755(1990).
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P13909;
01-JAN-1990
01-JAN-1990
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01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (
PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPIMEI OR PAII.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                EMBL; X16383; CAA34419.1; -.
EMBL; X55906; CA37094.1; -.
EIREL; S01324; S01324.
PIR; S06745; S06745.
PIR; S06745; S06745.
PIR; P01008; IATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>:</del>
PROSITE; PS00284; SERPIN; 1. Serpin; Serine protease inhibitor; Glycoprotein; Signal.
                                                                                   InterPro; IPRO00215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRINOLYSIS: PAIL IS INACTIVATED BY PROTEOLYTIC ATTACK OF MISCELLANEOUS: PAIL IS INACTIVATED BY PROTEOLYTIC ATTACK OF UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING TH 369(R)-370(M) BOND.
MISCELLANEOUS: VASCULAR ENDOTHELIAL CELLS MAY BE THE PRIMARY OF SYNTHESIS OF PLASMA PAI.
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content is not the statement is not removed. Usage by and ties requires a license agreement (See http://www.isb-send an email to license@isb-sib.ch).
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en activator
                                                    Plasma;
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                                                    Plasminogen activation;
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CARBOHYD
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CONFLICT
SEQUENCE
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13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINGGEN ACTIVATOR INHIBITOR-1 PRECURSOR (
PLASMINGGEN ACTIVATOR INHIBITOR) (PAI).
SERPINEI OR PAII OR PLANHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-87053819; PubMed-2430793;
MEDLINE-87053819; PubMed-2430793;
Pannekoek H., Veerman H., Lambers H., Diergaa
van Zonneveld A.-J., van Mourik J.A.;
"Endothelial plasminogen activator inhibitor
the Serpin gene family.";
EMBO J. 5:2539-2544(1986).
                                                                                                                                                                                                                                                                                                                                                                                Ginsburg D., Zeheb R., Yang A.Y., Rafferty U.M., Andreasen P.A., Nielsen L., Dano K., Lebo R.V., Gelehrter T.D.; Royal Cloning of human plasminogen activator inhibitor from endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDILINE-88000586; PubMed=2820474; MEDILINE-88000586; PubMed=2820474; Loskutoff D.J., Linders M., Keijer J., van Heerikhuizen H., Pannekock H.; "Structure of the human plasminogen act nonrandom distribution of introns."; Biochemistry 26:3763-3768(1987).
                                                                                                                                                                               Gene
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                            Strandberg L., Lawrence D., Ny T.;
"The organization of the human-plasminogen-activator-inhibitor-legene. Implications on the evolution of the serine-protease inhib
                                                                                                                                                                                                   "Structure and expression of the human activator inhibitor, PAI-1.";
Gene 84:447-453(1989).
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-90128289; PubMed-2612914
Follo M., Ginsburg D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-87058123;
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                                                                                                                               SEQUENCE FROM N.A. MEDLINE-89005111; Pubmed-3262512;
                                             [amily."
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11; Conser
                      Biochem. 176:609-616(1988)
                                                                                                                                                                                                                                                                                                                                                              Invest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=3097076;
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REACTIVE BOND.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
S-> L (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB
Pred. No. 0.0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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9053617333C7D130
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0.0017;
                                                                                                                                                                                                                                                  gene encoding plasminogen
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                                                                        inhibitor
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SEQUENCE FROM N.A.
MEDLINE-88243790; PubMed-3132455;
Van den Berg E.A., Koolstra T.,

Siemieniak D.R.

Promoter and

Bosma P.J., van den Slightom J.L.;

tructural

Biol.

Chem. gene

Cordes

SEQUENCE FROM N.A.

D

Submitted Pannekoek SEQUENCE

FROM N.A.

urokinase-type plasminogen
advanced ovarian cancer.";

collaboration

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SEQUENCE OF 20-402 FROM N.A. MEDILINE-86313660; PubMed=3092219; MEDILINE-86313660; PubMed=3092219; Ny T., Sawdey M., Lawrence D., Millan J.L., Loskutoff D.J.; Ny T., Sawdey M., Lawrence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 83:6776-6780(1986).
                                                                                          X-RAY CRYSTALLOGRAPHY (2.99 ANGSTROMS).
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MEDLINE-99148119; PubMed-10368279;
MEDLINE-99148119; PubMed-10368279;
Ginsburg D., Stein P.E., Pannu N.S., Carrell R.W.,
Ginsburg D., Lawrence D.A., Read R.J.;
"The active conformation of plasminogen activator target for drugs to control fibrinolysis and cell structure 7:111-118(1999).
                                                                                                                                                                                                                                                                                       "Interfering with the inhibitory mechanism of serpins: crystal structure of a complex formed between cleaved plasminogen activator inhibitor type 1 and a reactive-centre loop peptide."; Structure 6:627-636(1998).
                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
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Xue Y., Bjorquist P., Inghardt T., Linschoten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
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Mechanisms contributing to the conformational and functional
flaxibility of plasminogen activator inhibitor-1.";
Nat. Struct. Biol. 2:891-897(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-47 AND 364-402 FROM N.A.
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Andreasen P.A., Ricoto A., Welinder K.G., Douglas R., Sar
Nielsen L.S., Oppenheimer C., Blasi F., Danoe K.;
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terminal heterogeneity determined by protein and cDNA seq
FEBS Lett. 209:213-218(1986).
VARIANT THR-15.
MEDLINE-97337920; Pu
Turkmen B., Schmitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           x-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-92114970; PubMed-1731226;
Mottonen J., Strand A., Symersky J., Sweet R.M.,
Geoghegan K.F., Gerard R.D., Goldsmith E.J.;
"Structural basis of latency in plasminogen activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  un T.C., Kretzmer K.K.;
'cDNA cloning and expression
lnhibitor (PAI) related to a
FBBS Lett. 210:11-16(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEDLINE-87105925; PubMed-3026837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wature 355:270-273(1992).
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263:9129-9141(1988).
PubMed=9194591;
tt M., Schmalfel
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. в.,
  Trommler
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                                                                                                                    inhibitor 1, adhesion.";
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       L, X04429; CAA28025.1; ...

JL; M14083; AAA60008.1; ...

BL; X04729; CAA28442.1; ...

BL; X04729; CAA28442.1; ...

BL; X04729; CAA28442.1; ...

BL; X04729; CAA28442.1; ...

BL; M16006; AAA60009.1; JOI MBL; M22314; AAA60009.1; JOI MBL; M22315; AAA60009.1; JOI MBL; M22317; AAA60009.1; JOI MBL; M22319; AAA60009.1; JOI MBL; X13339; CAA31722.1; ...

EMBL; X13340; CAB51737.1; EMBL; X13341; CAB51606.1; EMBL; X13342; CAB51739.1; EMBL; X13342; CAB51739.1; EMBL; X13344; CAB51739.1; EMBL; X13344; CAB51739.1; EMBL; X13345; CAA31729.1; EMBL; X13346; CAA31729.1; EMBL; X13346; CAA31729.1; EMBL; X13347; CAA31200.1; EMBL; X13346; CAA31729.1; EMBL; X13764; CAA
  CHAIN
ACT_SITE
CARBOHYD
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"Mutational analysis of the genes encoding urokinase-type plasminoge activator (µPA) and its inhibitor PAI-1 in advanced ovarian cancer." electrophoresis 18:686-689(1997).

-i- FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH ACTIVATOR, UROKINASE, AND PROTEIN C. OTHER REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                               Glycoprotein;
                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                               SWISS-2DPAGE; PO5121;
                                                                                                                                                                                                                                                                 InterPro;
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MISCELLANGOUS: TWO TYPES OF PAI HAVE BEEN IDEN
ACID-STRALE GLYCOPROTEIN FOUND IN PLASMA AND P
ENDOTHELIAL, HEPATOMA, AND FIBROSARCOMA CELLS.
MISCELLANGOUS: VASCULAR ENDOTHELIAL CELLS MAY
OF SYNTHESIS OF PLASMA PAI.
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPA MAY FUNCTION AS A MAJOR CONTROL FIBRINOLYSIS.

DISEASE: HIGH CONCENTRATIONS OF THI WITH HUMAN THROWBOEMBOLIC DISEASE.

MISCELLANEOUS: PAII IS INACTIVATED UROKINASE-TYPE (U-PA) AND THE TISSU
                                                                                                                                                                                                                                                                                                                                      1A7C; 23-MAR-99
1B3K; 10-DEC-99
                                                                                                                                                                                                                                                                                                                                                                                    A26996; ITHUP1.
S02551; S02551.
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       24
369
232
288
352
                                                                                                                                                                                                                                    9; serpin;
                                                                                                                       Polymorphism;
1 23
                                                                                                                                                                    94; SERPIN; 1.
protease inhibitor;
                                                                                                                                                                                                                 SERPIN;
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     402
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288
352
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JOINED
JOINED
JOINED
JOINED
JOINED
  PLASMINOGEN ACTIVATOR 1
REACTIVE BOND.
N-LINKED (GLCNAC. ...)
N-LINKED (GLCNAC. ...)
N-LINKED (GLCNAC. ...)
                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATED BY PROTEOLYTIC ATTACK OF THE THE TISSUE-TYPE (TPA), CLEAVING THE
                                                                                                                                               Plasma; Plasminogen
; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIS PROTEIN
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     (POTENTIAL)
(POTENTIAL)
                                                                                                     INHIBITOR-1.
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PRESENTED PROCESS SEPERATE SEP
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Query Match
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CARBOHYD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleöstomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (PAI-1) (ENDOTHELIAL PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINE1 OR PAI1 OR PLANH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIG.
                                                                                                                                                                          Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                 Pfam; PF00079; serpin; SMART; SM00093; SERPIN
                                                                                                                                                                                                                                                                              EMBL; Y11347; CAA72182.1; -. HSSP; P01008; IATH. InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bijnens A.P., Knockaert I., Cousin E., Kruithof E.K.O., Declerck P Thromb. Haemost. 77:1046-1046(1997).

Thromb. Haemost. 77:1046-1046(1997).

FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN - ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITTER MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bijnens A.P., Knockaert I., Cousin 
"Expression and characterization of 
activator inhibitor-1.";
                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERRATUM
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                                                                                                                                                                                                                             PROSITE; PS00284; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thromb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97206538; PubMed-9157595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: PAII IS INACTIVATED BY PROTEOLYTIC ATTACK OF THE UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING THE 369(R)-370(M) BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMAPEEIIMDR 379
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N-LINKED (GLCNAC. . .) (PO'
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PLASMINOGEN ACTIVATOR INHIBITOR-1
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Pred.
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plasminogen
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MEDLINE-90130456; P
Bruzdzinski C.J., R
Gelehrter T.D.;
CARBOHYD
CARBOHYD
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                                                           ACT_SITE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR (PAI-1) (ENDOTHELIAL PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINE1 OR PAI1 OR PLANH1.
                                                                                                                                                                                                                                                                                       EMBL; J05206; AAA41796.1;
EMBL; M24067; AAA56856.1;
PIR; A35032; A35032.
HSSP; P01008; IATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zeheb R., Gelehrter T.D.;
"Cloning and sequencing of cDNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeheb R., Gelehrter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89211983; PubMed-3149611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and characterization of the rat plasminogen activator inhibitor-1 gene.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10116;
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                                                                                                                                                                                                                       InterPro; IPR000215; Serpin. fam; PF00079; serpin; 1. MART; SM00093; SERPIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH TPA MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF FIBRINOLYSIS.

MISCELLANEOUS: PAI1 IS INACTIVATED BY PROTEOLYTIC ATTACK OF THE UROKINASE-TYPE (G-PA) AND THE TISSUE-TYPE (TPA), CLEAVING THE DEVINANCE TYPE (G-PA)
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Riordan-Johnson
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                                                                                                                                                                                       inhibitor; Plasma; Plasminogen
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                  BY SIMILARITY.

PLASMINOGEN ACTIVATOR I
REACTIVE BOND.

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20-AUG-2001 (Rel. 40, Last annotation update)
GRPE PROTEIN (HSP-70 COFACTOR) (HEAT SHOCK PROTEIN
GRPE OR B2614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE-97349980; PubMed-9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Aiba H., Baba T., Hayashi K., Miki T., Mitsuhashi N.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
Yamagata S., Horiuchi T.;
*Construction of a contiguous 874-kb sequence of the Escherichia col
*Kl2 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.*;
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                    POSSIBLE FUNCTION.

MEDLINE-91187894; PubMed-1826368;

Liberek K., Marszalek J., Ang D., Georgopoulos C., 2

Liberek K. Marszalek J., Ang D. Georgopoulos C., 2

"Escherichia coli Dnad and GrpE heat shock proteins

"Escherichia coli DnaK.";

Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipinska B., King J., Ang D., Georgopoulos C., "Sequence analysis and transcriptional regulation coli grpE gene, encoding a heat shock protein."; Nucleic Acids Res. 16:7545-7562(1988).
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                       X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-97258949; PubMed-9103205;
Harrison C.J., Hayer-Hartl M., di Liberto M.,
                                                                                                                                                                                 FUNCTION, AND MUTAGENESIS.
MEDLINE-97045089; PubMed-8890154;
Wu B., Wawrzynow A., Zylicz M., G
"Structure-function analysis of t
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STRAIN=K12 / MG1655;
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Bacteria, Proteobacteria;
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Pred. No.
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                                                                                                                                                                                    Georgopoulos C.;
the Escherichia
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PARESTILLE PROPERTY OF THE PRO
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Best Local S
Matches 8
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EMBL; AE000347; AAC75663.1; -.
EMBL; D90088; BAA16498.1; -.
PIR; S01240; S01240;
PDB; 1DKG; 20-AUG-97.
SWISS-2DPAGE; P09372; COLI.
ECOZDBASE; B055-3; CTH EDITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAI1_MOUSE
P22777;
01-AUG-1991
01-AUG-1991
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASMINOGEN ACTIVATOR INHIBITOR-1 PRECURSOR ()
PLASMINOGEN ACTIVATOR INHIBITOR) (PAI).
SERPINE OR PAII OR PLANHI OR MRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOGene; EG10416; grpE.
InterPro; IPRO00740; GrpE.
Pfam; PP01025; GrpE; 1.
PRINTS; PR00773; GRPEPROTEIN.
PROSTTE; PS01071; GRPEP. 1.
Chaperone; Heat shock; 3D-structure; Complete SEQUENCE 197 AA; 21798 MW; CDC4CD9D0BAD4BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the ATPase domain of the molecular chaperone I Science 276:431-435(1997).

FUNCTION: STIMULATES, JOINTLY WITH DNAJ, TONAK. HELPS TO RELEASE ADP FROM DNAK THUS MORE EFFICIENTLY.
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                             <del>:</del>
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90158593; PubMed-2406566;
Prendergast G.C., Diamond L.E., Dahl D.,
"The c-myc-regulated gene mrl encodes pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
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                                                                                                                          FIBRINOLYSIS.

MISCELLANEOUS: PAIL IS INACTIVATED BY PROTEOLYTIC ATTACK OF THE UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING THE
                                                                           369(R)-370(M) BOND. SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                            Cell. Biol. 10:1265-1269(1990).
FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTVATOR. UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH TPA MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: BY THE SIGMA(32) SUBUNIT OF RNA POLYMERASE. SIMILARITY: BELONGS TO THE GRPE FAMILY.
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8; Conser
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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0.49;
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                                                                                                                                                                                                                                                                                                                                                                          Cole M.D.;
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                                                                                                                                                                                                                                                                                                                                                   activator inhibitor
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RECYCLE
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Query Match
Best Local S
Matches 7
P SEQUENCE OF 1-494 FROM N.A.

C STRAIN-ATCC 1908 / CB15;

X MEDITINE-98012985; pubmed-9352936;

X Steinman H.M., Fareed F., Weinstein L.;

Catalase-peroxidase of Caulobacter crescentus: function and ro

Stationary-phase survival.*;

J. Bacteriol. 179:6831-6836(1997).

C -1- FUNCTION: BITUNCTIONAL, EXHIBITING BOTH A CATALASE AND

BROAD-SPECTRUM PEROXIDASE ACTIVITIES.

C-1- CATALYTIC ACTIVITY: DONGR + H(2)O(2) - OXIDIZED DONOR + 2 H

C -1- COATALYTIC ACTIVITY: DONGR + H(2)O(2) - OXIDIZED DONOR + 2 H

C -1- COATALYTIC BY EXPOSURE TO HYDROGEN PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATA_CAUCR
031066;
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                           STRAIN-ACC 19089 / CB15;
STRAIN-ACC 19089 / CB15;
MEDLING-21173698; PubMed-11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J., Heidelberg J.F., Alley M.K.R., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.
Salzberg S.L., Shapiro L., Venter J.C., Fraser C.M.;
Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEROXIDASE/CAPALASE (EC 1.11.1.6) (CATALASE-PEROXIDASE).
KATG OR CC3043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Caulobacter crescentus
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PIR; A34761; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=69394;
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IPR000215; Serp
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24 402
59 370
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NA; 45170 b
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Pred. No.
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REACTIVE BOND.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
765FF1659C70F68C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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Matches 7
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EMBL; AF027168; AAC43850.1; -.
HSSP; P48514; 1APX.
TIGR; CC3044; -.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002016; Peroxidase; 1.
PR0SITE; PS00436; PEROXIDASE_1; 1.
PR0SITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPH5_THIVI
P45365;
01-NOV-1995
01-NOV-1995
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
ACT_SITE
ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N. A.
STRAIN-2311 / DSN 208;
STRAIN-2511 / DSN 208;
MEDLINE-93159750; PubMed-7763384;
Liebergesell M., Steinbuechel A.;
Liebergesell M., Steinbuechel A.;
"Cloning and molecular analysis of the poly(3-hydroxybutyric acid)
biosynthetic genes of Thiocystis violacea.";
biosynthetic genes of Thiocystis violacea.",
Appl. Microbiol. Biotechnol. 38:493-501(1993).
1- SIMILARTTY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 76.5 KDA PROTEIN IN PHBC 3'REGION (ORF5).
Thiocystis violacea.
Bacteria, Proteobacteria; gamma subdivision; Chromatiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (see http://www.isb-sorsend.an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thiocystis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601 MAPEEALVDR 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 70.
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102
106
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737 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
106
268
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70.0%;
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BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
D900742D04E02E97 CRC64;
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EMBL; L01113; AAB02863.1; -. EMBL; S54369; AAC60431.1; -. InterPro; IPR001633; DUF2. InterPro; IPR000160; DUF9. InterPro; IPR0001789; Response

Response_reg

an email to license@isb-sib.ch).

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AVILES E., Berno A., Brennan T., Carpenter J., Chen E., Araujo R.,
RA Chung E., Duncan M., Guzman E., Hattzell G., Hunicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lashkari D., Kayser S., Kayser C., Lashkari D., Las
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLN3_YEAST STANDARD; PRT; 7
P18494;
01-NOY-1990 (Rel. 16, Created)
01-FEB-1995 (Rel. 31, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
          EMBL; M35267; AAA34645.1;
EMBL; U18796; AAB64575.1;
PIR; S22280; S22280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein;
MOD_RES 188 18
SEQUENCE 692 AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
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Pfam; I
SMART;
                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Dietrich F.S., Mulligan J.T.,
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NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence and expression of GLN3, a pof Saccharomyces cerevisiae encoding finger DNA-binding domain.";
Mol. Cell. Biol. 11:6216-6228(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minehart P.L., Magasanik B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 RLAPEVVILD 58
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les 6; Conser
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n; PF0072; response_reg; 1
RT; SM00267; DUF1; 1.
RT; SM00052; DUF2; 1.
RT; SM00448; REC; 1.
                                                                                                             an
                                                                                                                                    requires a
                                                                                     equires a license agreement (See http://www.isb-slb.ch/announce/email to license@isb-slb.ch).
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; 76476 MW;
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B PHOSPHORYLATION (BY SIMILARITY).
6476 MW; F6B80E63F44E11F7 CRC64;
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Pred. No. 20;
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on update)
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RESULT
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Best Local S
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InterPro; IPR000679; i
Pfam; PF00320; GATA;
PRINTS; PR00619; GATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPOL_CHVN2
P30320;
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CHVN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                              PRINTS; PR00106; DNAPOLB.
SMART; SM00466; POLBC; 1.
PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Hydrolase; Nuclease; Exonuclease; Multifunctional enzyme;
                                                                                                                                                                                                                                                             EMBL; M86837; AAA88827.1; -. PIR; B42543; B42543.
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updato)
DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0619; GATARNEINGER.
SMART; SM00401; ZnF_GATA; 1.

PROSITE; PS00344; GATA_ZN_FINGER_1; 1.

PROSITE; PS50114; GATA_ZN_FINGER_2; 1.

Transcription regulation; Activator; DNA-binding; Zinc-finger;
                                                                                                                                                                                                                PIR; B42543; B42543.
InterPro; IPR002064; DNA_pol_B.
Pfam; PF00136; DNA_pol_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no NCBI_TaxID=12619;
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlorella virus NY-2A (CV-NY2A).
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                                                                    Early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N PYROPHOSPHATE + DNA(N).
-I- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
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351
474
730 AA;
     913 AA;
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361 A
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     MW.
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Pred. No. 3
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P -> G (IN REF. 1).
; 3159E1844469942E CRC64;
CONTAINS CONSERVED RESIDUES ESSENTIAL 3' -> 5' EXONUCLEASE ACTIVITIES. 7: 7E656423123B02B5 CRC64;
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01-OCT-1994
20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-93212587; PubMed-8460526; Accardi L., Gro M.C., dl Bonito P., Glorgi C.; *Toscana virus genomic L segment: molecular cloning, coding strategy and amino acid sequence in comparison with other negative strand RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toscana virus (Tos).
Viruses; ssRNA negat
NCBI_TaxID=11590;
SEQUENCE FROM N.A.
STRAIN-812 / MGI65;
MEDLINE-93347969; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; Sale Nuclear Transferase; Nuclear 2095 AA;
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-I- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                       P32125; P76770;
01-OCT-1993 (Re
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(Rel. 30, Last sequence update)
(Rel. 40, Last annotation updat
D RNA POLYMERASE (EC 2.7.7.48) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotidyltransferase; RNA-directed 095 AA; 238885 MW; 22FF4DAD745583B7
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Mismatches
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      Blattner F.R.;
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Best Local S
Matches 5
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061820;
01-NOV-1997
01-NOV-1997
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GTP-BINDING
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NP_BIND
SEQUENCE
   MEDLINE-95152168; PubMed-7849398; COULAVAS E.E., HSieh C.M., Ren M., D'Eustachio P.D.; D'Eustachio P.D.; The Medical P.D
                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
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5; Conserv
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(Rel. 35, Last sequence update)
(Rel. 37, Last annotation update)
NUCLEAR PROTEIN RAN, TESTIS-SPECIFIC
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GTP (POTENTIAL).
GTP (POTENTIAL).
W; C3522F4DFBF3833C (
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                                                                                                                                                                                                                                                                                                                                        Taves D.J., Palmer T., Boxer D.H.;

"The product of the molybdenum cofactor gene mobb of Es
is a GTP-binding protein.";

EUX. J. Biochem. 246:690-697(1997).

-1- FUNCTION: MAY BIND THE GUANINE NUCLEOTIDE REQUIRED

SYNTHESIS OF MOLYBDENUM COFACTOR BIOSYNTHESIS.

-1- PATHMAY: MOLYBDENUM COFACTOR BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of the Escherichia coli genome. region from 87.2 to 89.2 minutes."; Nucleic Acids Res. 21:3391-3398(1993). [2]
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InterPro; IPR003755; Small_GTPase.
Pfam; PF00071; ras; 1.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                  SEQUENCE FROM N.A.
MEDLINE-92339546; PubMed-1633874;
Trueb J., Trueb B.;
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SMART; SM00010; small_GTPase;
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Q91kK7 arabidopsis
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19SGC8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T23G18.18.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosidae; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
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InterPro; IPR000379; ESK_Lip_thioest_actsite.
SEQUENCE 382 AA; 43223 MN; 353040AF91BC84E0 CRC64;
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Nature 409:1007-1011(2001).
EMBL, ALSB3919; CAC30290.1; -.
InterPro; IPR000309; TrkA_Kuptake.
Pfam; PF02080; TrkA; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, HYPOTHETICAL PROTEIN ML0781.
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Cole S.T., Eiglmeier K., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9U1B4 PRELIMINARY; PRT; 329 AA.
Q9U1B4; O19U1B4; O29U1B4;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POSSIBLE BETA PROPELLER PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
Zimmermann W., Hambutt R., I
Rajandream M.A., Barrell B.C
Submitted (DEC-1999) to the
                                                                        "A physical map of the Leishmania major Genome Res. 8:135-145(1998).
EMBL; AL121851; CAB58300.1; -.
InterPro: IPR001680; WD40.
Pfam; PF00400; WD40; 3.
SMART; SM00320; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major
Eukaryota: Euglei
                                                                                                                                                                                                                                                                                                                             Ivens A.C.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98146435; PubMed+9477341; Ivens A.C., Lewis S.M., Bagherzadeh A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5664;
                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
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    PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ivens A.C.,
.G.;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawson
                                                                                                                                                                                                                                                                                                  Friedlin genome.";
                                                                                                                                                                                                                                                                                                                                                                           Zhang L., Chan H.M.,
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Best Local S
Matches 5
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Best Local S
Matches 6
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
BETA 1,2-XYLOSYLTRANSFERASE.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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SEQUENCE
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BETA1,2-XYLOSYLTRANSFERASE (GENOMIC DNA, CHROMOSOME
CLONE:MTE17).
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STRAIN-CV, WS;
GOMORD V., Baltresca V., Kiefer-Meyer M.-C., Faye L.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF272852; AAF77064.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9LKK7
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SEQUENCE 533 AA;
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear crees).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0H016
                                                     SEQUENCE FROM N.A. Bakker H.;
                                                                                                                              Steinkellner H.; "Molecular cloning and functional expression of beta "Molecular cloning and from Arabidopsis thallana."; xylosyltransferase cDNA from Arabidopsis thallana."; FEBS Lett. 472:105-108(2000).
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20245450; PubMed-10781814;
Strasser R., Mucha J., Mach L., Altmann F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
"Arabidopsis cDNA for betal,2-xylosyltransferase.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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6; Conserva
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Pred. No.
2; Mismatcl
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Pred. No. 79;
4; Mismatches
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                                                                                                                                                                                                                                          Wilson I.B.H.,
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RESULT
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Best Local S
Matches 6
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Best Local Similarity 50.0
Matches 5; Conservative
O990L6 PRELIMINARY;
O990L6;
O1-JUN-2001 (TrEMBLrel. 17, C)
O1-JUN-2001 (TrEMBLrel. 17, I)
O1-JUN-2001 (TREMBLrel. 17, II)
ONA POLYMERASE (FRAGMENT).
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01-MAY-2000
01-JUN-2001
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Q9R708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO02016; Peroxidase.
InterPro; IPRO01680; MD40.
InterPro; IPRO01680; MD40.
Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE; UNKNOWN_1.
PROSITE; PS00678; MD_REPRINTS_1; UNKNOWN_1.
SEQUENCE 723 AA; 78741 MW; AA531987F535B508 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xu x.Q., Pan S.Q.;
*An Agrobacterium catalase is a virulence factor
tumorigenesis.";
**Pan original factor factor functions for the factor facto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase.
SEQUENCE 534 AA;
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EMBL; AJ272121; CAB90610.1; -.
EMBL; AJ277603; CAB89489.1; -.
EMBL; AB015479; BAB08567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium radiobacter.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Microbiol. 0:0-0(1999).
EMBL; AB033631; BAA89349.1; -.
HSSP; P48534; 1APX.
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Nakamura Y., Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM
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S., Asamizu E., Kaneko
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Paramecium bursaria chlorella v
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Zhang Y., Adams B., S
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viruses.";
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Paramecium bursaria chlorella virus 1 (PBCV-1).

Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae;

NCBI_TaxID=10506;
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"Intron conservation
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STRAIN-AR158;
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Viruses; dsDNA viruses,
NCBI_TaxID-10506;
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099013;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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SEQUENCE
                                                                                                                                                                                                                                                                                                                             O30043 PRELIMINARY; PRT; 540 AA.
O30043; O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEDIUM-CHAIN ACYL-COA LIGASE (ALKK-1).
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SEQUENCE FROM N.A.
STRAIN-WC-16 / DSM 4304 / ATCC 49558;
STRAIN-B-98409343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang Y., Adams B., :
"Intron conservation viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-NYS-1;
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus
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"Intron conservation in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-NY-2B;
                                                                                                                                                                                                Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2001) to the EMBL; AF344235; AAK28956.1;
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                                                                                                                                                              NCBI_TaxID=2234;
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220 AA;
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24927 MW;
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       Tomb J.-F.,
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Pred. No. 80;
4; Mismatches
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DNA polymerase gene encoded by Chlorella
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DNA polymerase gene encoded
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       Nelson K.E.,
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Matches 6; Conservative
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Matches 6; Conserv
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Q9QSK5;
01-MAY-2000
01-MAY-2000
01-MAY-2000
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        OSFOL8 PRELIMINARY; PRT; 691 AA.

OSFOL5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTAMATE SYNTHASE LARGE SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Muller K., Tidona C.A., Bahr U., Darai G.;

"The DNA sequence of Chilo iridescent virus
coordinates 0.974 and 0.101.";

Submitted (AUG-1998) to the EMBL/GenBank/DDB
EMBL; AF083915; AAD48147.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                       Chilo iridescent virus Viruses; dsDNA viruses, MSDNA viruses, NCBI_TaxID=10488;
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                                                                                                                                                                                                                                                                                             SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
EXONUCLEASE II HOMOLOG.
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Pred. No. 2.1e+02;
2; Mismatches C
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Pred. No. 2.4e+02;
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Best Local Similarity 50.0
Matches 5; Conservative
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TISSUE-BRAIN;

MEDLINE-20181126; PubMed-10718198;

MEDLINE-20181126; PubMed-10718198;

Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;

Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;

Prediction of the coding sequences of unidentified human

The complete sequences of 150 new cDNA clones from brain w

for large proteins in vitro.";

DNA Res. 7:65-73(2000).

EMBL; AB037824; BAA92641.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
BOYLE-Vavra S., Ebert C.E., Daum R.S.;
Boyle-Vavra S., Ebert C.E., Daum R.S.;
The gltB gene encoding the large (a) subunit of glutamate synthase identified by screening a vancomycin-resistant Staphylococcus aureus library on medium containing vancomycin.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF217184; AAG44102.1; ...
BONLTER 1 1 1 1 61 1 NON TER 691 601
GLTB OR SA0430.
Staphylococcus aureus
Bacteria; Firmicutes;
                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GLUTAMATE SYNTHASE LARGE SUBUNIT.
                                                                                             Q99WD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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O1-CCT-2000 (TrEMBLrel. 15,

O1-CCT-2000 (TrEMBLrel. 15,

O1-CCT-2000 (TREMBLrel. 15,

KIAA1403 PROTEIN (FRAGMENT)
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID-1280;
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subsp. aureus N315.
Bacillus/Clostridium
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                                                                                                             1499 AA.
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5.5e+02;
group;
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SEQUENCE FROM N.A.

KUTODA M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekinizu K.,

Takahashi N.K., Sawano T., Sabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

Ogassara N., Hayashi H., Hiramatsu K.;

Ogassara N., Hayashi H., Hiramatsu K.;
                                                                                                                                        "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
Lancet 357:1225-1240(2001).
EMBL, AP003130; BAB41660.1;
COMPLETE PROTECOMP.
COMPLETE PROTECOMP.
1499 AA; 166259 MW; F20B82287BCF001C CRC64;
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NCBI_TaxID=158879;
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Pred. No. 6.
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Plasminogen activa Plasminogen activa

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GTP-binding

Plasminogen Activa

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Gapop 10.0 , Gapext 0.5
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29
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                                                                                                                        Length
                                                                                                                        DB
   chosen parameters:
                                                                                                                        ijΒ
  AAY01812
AAY42738
AAB92200
AAG32040
AAG32040
AAG32039
AAR11756
AAR12162
AAR12163
AAR12163
AAR1216710
Peptide used to re
Human alpha-1-anti
Thrombin inhibitor
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Human PAI-1 P1-P1'
Human PAI-1 P2-P2'
Human PAI-1 P3-93'
Plasminogen activa
                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                             RESULT
AAY01812
   Abnormal cell migration; PAI-1-dependent cell adhesion; scuPA clearance; pathological cell migration; angiogenesis; organogenesis; ovulation; inflammation; cancer; tumor cell invasion; metastasis; atherosclerosis.
           Example 1; Page 31; 63pp; English
                                                                      Cines D,
                                                                                         (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                      Peptide used to regulate scuPA.
                                                                                                                                                                                                                                                                           29-JUN-1999
                             Peptide composition
                                                   WPI; 1999-288168/24
                                                                                                               17-OCT-1997;
                                                                                                                                 15-OCT-1998;
                                                                                                                                                      29-APR-1999
                                                                                                                                                                         WO9920295-A1
                                                                                                                                                                                                                                                                                                 AAY01812;
                                                                                                                                                                                                                                                                                                                    AAY01812 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    Higazi AA;
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                                                                                                               97US-0062274
                                                                                                                                  98WO-US21800
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AAR07986
AAW31587
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AAB90794
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AAG37027
AAG55451
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AAB68542
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AAU04929
AAR08411
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AAU04923
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AAU04921
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AAW26713
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This sequence represents human alpha-1-antitrysin cterminal peptide fragment 6. Alpha-1-antitrypsin is a known inhibitor of serine proteases, but loses its inhibitory activity due to a change in tertiary structure when cleaved by proteases such as leukocyte elastase. The cleaved alpha-1-antitrypsin molecules are cleared from the circulation through receptors in the liver and is accompanied by a depletion of extracellular cholesterol. The cause of this cholesterol depletion is due to an increase in the number of low density lipoprotein (LDL) receptors in liver cells which take up the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-1-antitrypsin; fragment; low density lipoprotein; LDL; latherosclerosis; gallstone.
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                                                                                                                                                                                                                                                                                                                                    Lowering cholesterol levels in a patient using hypocholesterolemic peptide \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VIRGINIA COMMONWEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1998;
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                                                                                                                                                                                                                                                                                Disclosure; Page 5; 28pp;
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1 eeiimd 6
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myristoylated, benzoylated or carbobenzoxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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LDL; LDL receptor;
                                                                                                                                                                                                                                                                                   English.
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. 4.3e+05;
ches 0;
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hypercholesterolaemia;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDL cholesterol complex. This invention takes advantage of the fact that there is an increase in LDL receptor levels induced by the presence of cleaved alpha-1-antitrypsin and it derivatives, including C-terminal peptide fragments. The C-terminal peptide fragments (AAY42733-Y42749) can be used to reduce the levels of LDL cholesterol in a patient and can be used to treat a wide variety of disorders, including atherosolerosis, hypercholesterolaemia and gallstones. As the peptides are derived from a naturally occurring human serum protein, they should not produce immune
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various dispraces. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or
                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protection; endogenous therapeutic peptide; peptidase; cor
blood component; modification; succinimidyl; maleimido gro
hydroxyl; thiol; hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB92200 standard; Peptide; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         side effects.
                                                                                                                                                                                                           Disclosure; Page 646; 733pp; English.
                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                        Bridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombin inhibitor peptide SEQ ID NO:1376.
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ilarity 100.0%;
Conservative
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99US-0153406.
99US-0159783.
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RESULT AAG32041 ID AAG3204 ID AAG320
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
25-MAR 1999
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06-PR 1999
16-APR 1999
16-APR 1999
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24-MAY 1999
14-MAY 1999
19-MAY 1999
21-MAY 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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9908-0121825
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0; Mismatches
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14-JUN-1999

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Best Local Similarity 100.0%; 1
Matches 6; Conservative 0;
28-APR 1999
30-APR 1999
30-APR 1999
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05-MAY 1999
06-MAY 1999
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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990S-0125488

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990S-0128214

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16-SEP-1999
20-SEP-1999
21-SEP-1999
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Matches 6
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h 100.0%;
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                            9908-0147935.
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9908-0161106.
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  Score 29; DB
Pred. No. 53;
0; Mismatches
                21;
   0
                Length
    Indels
                 236;
   0
    Gaps
    0
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10-JUN 1999
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    9908-012386

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9908-012578

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AAR11756
ID AAR11756 standard; Protein; 379 AA.
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Matches 6
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence comprises mature PAI-1 in which Met(347) from the reactive centre (SGTVAGSSTAVIVSARMAPERIMD) has been replaced by Ser from the corresponding site of ATIII. The mutant PAI-1 is used to prevent reocclusion. It binds to vitronectin to act as a strong thrombin inhibitor, but is much less effective as a PA inhibitor. See also AAR11755 and AAR12162-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New plasminogen activator inhibitor 1 (PAI-1) mutants - comprise region of antithrombin III (ATIII), useful in fibrinolytic-thrombolytic therapy
          03-OCT-1989;
                                               03-OCT-1990;
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                    plasminogen activator inhibitor; antithrombin III; vitronectin; fibrinolysis; thrombolysis; serpin.
                                                                                                                                                                                                                                                              Human PAI-1 P2-P2' ATIII mutant.
                                                                                                                                                                                                                                                                                                        10-JUL-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                             AAR12162;
                                                                                                                                                                                                                                                                                                                                                                                AAR12162 standard; Protein; 379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 24; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-132855/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pannekoek H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STCL ) STICHT INST AND BLOEDTRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasminogen activator inhibitor; antithrombin III; vitronectin;
fibrinolysis; thrombolysis; serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PAI-1 P1-P1' ATIII mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-1991
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                                                                                    16-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Pred. No. 84;
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84;
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Best Local S
Matches 6
This sequence comprises mature PAI-1 in which residues 344-349 (1.e.SerAlaArgMetAlaPro) in the reactive centre has been replaced by AlaGlyArgSerLeuAsn from the corresponding site of ATII. The mutant PAI-1 is used to prevent reocclusion. It binds to vitronectin to act as a strong thrombin inhibitor, but is much less effective
                                                                                   New plasminogen activator i region of antithrombin III thrombolytic therapy
                                                                 Claim
                                                                                                                                                                                                03-OCT-1989;
                                                                                                                                                                                                                      03-OCT-1990;
                                                                                                                                                                                                                                                                                                                                         Human PAI-1 P3-P3'
                                                                                                                                                                          (STCL ) STICHT
                                                                                                                                                                                                                                          18-APR-1991
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                 plasminogen activator inhibitor; antithrombin III; vitronectin;
                                                                                                                                                                                                                                                                                                                                                             10-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                   AAR12163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence comprises mature PAI-1 in which residues 345-348 (1.e.AlaArgWetAla) in the reactive centre has been replaced by GlyArgSerLeu from the corresponding site of ATIII. The mutant PAI-1s used to prevent reocclusion. It binds to vitronectin to act as strong thrombin inhibitor, but is much less effective as a PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New plasminogen activator inhibitor 1 (PAI-1) mutants - comprise region of antithrombin III (ATIII), useful in fibrinolytic-thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                       AAR12163 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-132855/18
                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                        ibrinolysis;
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                                                                                                                                1991-132855/18
                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Page 24; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 AA;
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                              24; 32pp;
                                                                                                                                                                                                                                                                                                         thrombolysis; serpin.
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                                                                                                                                                                                                                                                                                                                                        ATIII mutant.
                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                English.
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                                                                                              c inhibitor
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Pred. No.
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Mismatches
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                                                                                               1 (PAI-1)
useful in
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                                                                                               mutants - comprise
fibrinolytic-
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human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has an Ala for Arg substitution at amino acid cresidue 346, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAW36710-25) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may have additional stabilising mutations comprising between one and four of His-50, Thr-154, Leu-319 and Ide-354, and one or more of Arg-333, Arg-335, Gly-331, Ile-372 and Leu-91. The mutants are characterised by being resistant to inactivation by elastrase, plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A and B, stromelysin and collagenase, and by having a high affinity that thoological elastase activity (specifically in emphysema, adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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See also
                                                                                                                                                                                                                                                    Claim 4; Page -; 144pp; English.
                                                                                                                                                                                                                                                                                Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; neointina; fibrosis; wound healing; tumour; metastasis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasminogen activator inhibitor type 1; PAI-1; human; elastase; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome; acute lung inflammation; alpha 1-antitrypsin deficiency;
                                                                                                                                                                                                                         This polypeptide comprises a preferred mutant, PlAla (R346A),
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor.
b AAR11755-6 and AAR12162
                                                                                                                                                                                                                                                                                                                                                                      DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activator inhibitor mutant PlAla (R346A).
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                                                                                                                                                                                                                                                                                                                                                                       Stefansson SP;
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RESULT 11
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Best Local S
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Synthetic.
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                                                     plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
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   Claim
                                                                                                                                                                                 WPI; 1997-526399/48.
                                                                                                                                                                                                                                           Lawrence DA,
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Pred. No.
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                      plasminogen activator inhibitor type 1; PAI-1; human; elastas; inhibitor; vitronectin; cell attachment; cell migration; cell proliferation; emphysema; adult respiratory distress syndrome acute lung inflammation; alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; panocreatitis; periodontal disease; arthritis; HIV; atherosclerosis; restenosis; periodontal disease; arthritis; HIV; atherosclerosis; psoriasis; neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
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                                                                                                                                                                           Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activator inhibitor mutant P1Gly (R346G).
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AAW26713
ID AAW2
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                  Plasminogen activator inhibitor
                                                             14-APR-1998
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350 eeiimd 355
                                                                                                    AAW26713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adaptation of the specification).
                                                                                                                                      AAW26713 standard;
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                                                                                                                                                                                                                                                                                                                            Conservative
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o acid sequence of the mutant protein was obtained by the wild-type sequence provided in Fig 4A of the
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                                                                                                                                          Protein;
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Pred. No. 84;
                  mutant Plasp (R346D)
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This polypeptide comprises a preferred mutant, Plasp (R346D), of CC human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31887). It has an Asp for Arg substitution at amino acid CC residue 346, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA CC (see AAW19730) and expression in a host cell. Claimed PAI-1 mutants (see AAW19730) and expression in a host cell. Claimed PAI-1 mutants (comparision 343-350, especially at position 343 and/or 346, and may CC have additional stabilising mutations comprising between one and CC four of His-150, Thr-154, Leu-319 and Ine-354, and one or more of CC plasminogen activator, plasmin, cathepsin G, chymase, gelatinases a CC and B, stromelysin and collagenase, and by having a high affinity CC pathological elastase activity (specifically in emphysema, adult CC respiratory distress syndrome, acute lung inflammation, congenital cathepsin G, chymase, gelatinases a CC alpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, CC pancreatitis, periodonntal disease, arthritis and HIV infection), CC migration-induced proliferation (specifically in emphysema, adult craspinatory distress syndrome, acute lung inflammation, congenital CC alpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, CC pancreatitis, periodonntal disease, arthritis and HIV infection), They also inhibit Vn-stimulated cell attachment, migration and/or Migration-induced proliferation (specifically in atherosclerosis, CC migration induced proliferation (specifically in atherosclerosis, CC condition involving pathological angiogenesis (all claimed). Since the mutants are resistant to cleavage by the proteases to which they are more effective therapeutic agents. They also condition involving pathological angiogenesis (all claimed). Since the sunday are more effective therapeutic agents. They also condition in the condition of eleatance of elastase (or its complex with PAII-1) CC pathological angiogenesis (all claime
                                             by receptors.

(NB. the amino acid sequence of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the specification).
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Sequence
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Query Match Best Local S Matches 6

h 100.0%; Score 29; DB Similarity 100.0%; Pred. No. 84; 6; Conservative 0; Mismatches

DB 18; 34; 38 0;

Length 379; Indels

0; Gaps

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RESULT ANAW26714 ANAW26714
CC This polypeptide comprises a preferred mutant, P4Ala (V343A), of CC Inman plasminosen activator inhibitor (PAI-1) mature protein (see CI also AAW31387). It has an Ala for Val substitution at amino acid CC residue 343, i.e. in the reactive centre loop of the protein. The mature AMP37303 and expression in a host cell Claimed PAI-1 mutants CC (see AAW26710-25) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may CC have additional stabilising mutations comprising between one and CC Arg-333, Arg-333, Gly-331, Ile-372 and Leu-91. The mutants are CC characterised by being resistant to inactivation by elastase, CC plasminogen activator, plasmin, cathepsin G, chymase, gelatinases A CC and B, stromelysin and collagenase, and by having a high affinity CC pathological elastase activity (specifically in emphysema, adult CC respiratory distress syndrome, acute lung inflammation, congenital CC alpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, periodontal disease, arthritis and HIV infection). They also inhibit Vn-stimulated cell attachment, migration and/or mayartion-induced proliferation (specifically in atherosclerosis, CC trauma, vascular graft restenosis, fibrosis (associated with cc chronic inflammation or chemotherapy, or of the lung), wound cc healing with scarring and fibrosis, growth/invasion of primary
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasminogen activator inhibitor type 1; PAI-1; human; elastas; inhibitor; vitronectin; cell attachment; cell migration, cell proliferation; emphysema; adult respiratory distress syndrom acute lung inflammation; alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis; pancreatitis; periodontal disease; arthritis; HV; atherosclerosis; restenosis; periodontal disease; arthritis; HV; atherosclerosis; propositions; fibrosis; wound healing; tumour; metastasis; psoriasis
This polypeptide comprises a preferred mutant, P4Asp (V343D), of human plasminogen activator inhibitor (PAI-1) mature protein (see also AAW31587). It has an Asp for Val substitution at amino acid residue 343, i.e. in the reactive centre loop of the protein. The mutant can be obtained by site-directed mutagenesis of PAI-1 DNA (see AAW367302) and expression in a host cell. Claimed PAI-1 mutants (see AAW367302) have at least one amino acid substitution at position 343-350, especially at position 343 and/or 346, and may have additional stabilising mutations comprising between one and
                                                                                                                                                                                          Plasminogen activator-inhibitor type I mutant inhibits elastase has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
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                                                                                                                                                               Claim
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is complex with PAI-1)
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CC four of His-150, Thr-154, Leu-319 and Ile-354, and one or more of CC characterised by being resistant to inactivation by elastase, CC plasminogen activator, plasmin, cathepsin G. Chymase, gelatinases A CC and B. stromelysin and collagenase, and by having a high affinity CC for vitromectin (Yn) and are used, in vivo or in vitro, to inhibit CC pathological elastase activaty (specifically in emphysema, adult CC respiratory distress syndrome, acute lung inflammation, congenital CC alpha 1-antitrypsin deficiency, cystic fibrosis, atopic dermatitis, periodontal disease, arthritis and HIV infection). CC migration-induced proliferation (specifically in atherosclerosis, constraints) periodontal disease, arthritis and HIV infection). CC migration-induced proliferation (specifically in atherosclerosis, constraints) are resistant to community in atherosclerosis, condition inflammation or chemotherapy, or of the lung), wound channed in inflammation or chemotherapy, or of the lung), wound condition involving pathological angiogenesis (all claimed). Since they bind, they are more effective therapeutic agents. They also promote uptake and clearance of elastase (or its complex with PAI-1) by receptors.

Query Match and clearance of the mutant protein was obtained by adaptation of the wild-type sequence provided in Fig 4A of the Securities of the wild-type sequence provided in Fig 4A of the Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; buther in the Security of the wild-type sequence provided in Fig 4A of the Search completed: March 18, 2002, 09:48:56
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/DGTUS_COMB.pep:*
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US-09-038-935-6
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US-08-477-112-6
US-08-477-112-6
US-08-477-112-6
US-08-915-461-7
US-08-948-997-4
US-08-948-997-4
US-08-948-997-9
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US-09-196-520-8
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TOPOLOGY: lin
MOLECULE TYPE:
US-08-781-020-6
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MEDIUM TYPE: F10Ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELease #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,020
FILING DATE: 09-JAN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E
REGISTRATION NUMBER: 22,635
REFERENCE/DOCKET NUMBER: VCU-16
TELEPHONE: 703-391-2510
TELEPHONE: 703-391-2510
TELEPHONE: 703-391-035
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
STRANDEDNESS:
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US-08-781-020-6
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Matches 6
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Patent No.
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ADDRESSEE: WHITHAM, CURTIS, WHITHAM & MCGINN
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wright, H.
TITLE OF INVENTION: ME
TITLE OF INVENTION: DE
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
     EEIIMD
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Similarity 100.0%;
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US-08-316-001A-12
US-08-611-928-10
US-09-173-891-10
US-09-076-137-12
PCT-0592-03624-12
US-08-481-700B-8
US-09-07--83-16
US-09-07--83-16
US-08-48-7-366-2
US-08-48-7-366-2
US-08-48-7-366-2
US-08-48-7-46-8
US-08-48-7-46-8
US-08-48-7-20
US-08-48-7-20
US-08-48-7-20
US-08-48-7-20
US-08-48-7-36-9
US-08-48-7-36-9
US-08-48-7-36-9
US-08-48-7-36-9
US-08-48-7-36-9
US-08-48-7-48-8
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Result No.

Score

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-038-935-6
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                                                             NAME: LIVNAT, SHMUEL

REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 3080
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 882-0168
TELEFAX: (202) 882-016
TELEFAX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Janciauskiene, Sabina
APPLICANT: Janciauskiene, Sabina
TITLE OF INVENTION: LIPOPROTEIN CHOLESTEROL
FILE REFRENCE: 294022ba
CURRENT APPLICATION NUMBER: US/09/038,935
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 08/781,020
EARLIER APPLICATION NUMBER: 08/781,020
EARLIER FILING DATE: 1997-01-19
NUMBER: OF SEQ ID NOS: 17
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tent No. 610349
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tent No. 615033
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                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT: LAWRENCE, DANIEL A.
PPLICANT: STEFANSSON, STEINGRIMUR P.
PTLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
PTLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSER
STREET: 2000 PENNSYLVANIA AVENUE, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEIIMD 6
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4 EEIIMD 9
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STRANDEDNESS:
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                      : 379 amino acids
amino acid
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RESULT 5
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US-08-121-714-6
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LEGITH: 390
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Best Local Similarity
Matches 6; Conserv
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APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 50. or 555X
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WORDERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sager,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quence 6, Application US/08121714 tent No. 5470970
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADU...
STREET: L.
STREET: Massar
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                                                          373 EEIIMD 378
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les 6; Conserv
                                                                          1 EEIIMD 6
                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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225 Franklin Street
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Pred. No.
                                                                                                                                   Score 29; DB 1;
Pred. No. 37;
                                                                                                                     Mismatches
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VERAL INFORMATION:

Application US/08477108A 5801001

TTLE OF INVENTION: MASDIN, A NOVEL SERDIN WITH

Anisowicz,

Anthony

OF SEQUENCES:

Fish & Richardson P.C.

Franklin Street

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Length 390;
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Best Local Similarity 100.0
***Tches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application PC/TUS9308322
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION.
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ANDRESSEE: Fish & Richardson
ANDRESSEE: Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 390
TYPE:
FILING DAYS.

FILING DAYS.

CLASSIFICATION:

CLASSIFICATION DATA:

APPLICATION NUMBER: 07/6

APPLICATION NUMBER: 09/01/92
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                  SOFTWARE: WORDPERIECT CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.C. COUNTRY: U.C. 2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/
FILING DATE: 09/01/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 EEIIMD 378
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                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 06
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER | PROPERTY | PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02/28/91
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: (FILING DATE: 02/28/91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
FILING DATE: 02/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Y: U.S.A.
                                                                                                                                                                                                                         WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PS/2 Model
SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02/28/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Janis K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                    PCT/US93/08322
                                                 07/938,823
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50Z or 55SX
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JS-08-477-112-6

373 EEIIMD 378

1 EEIIMD 6

Query Match Best Local Matches

Local Similarity

100.0%; Score 29; 100.0%; Pred. No.

6;

Conservative

NFORMATION FOR SEQ ID NO:

6.

TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070

REFERENCE/DOCKET NUMBER: REGISTRATION NUMBER: 1

34,819

06570/002002

felefax:

FILING DATE: 02/28/91 ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER

02/28/92

07/662,216 07/844,296

PPLICATION NUMBER: PPLICATION NUMBER: 0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: June 7, 1995
CLASSIFICATION: 536

US/08/477,108A

FIOR APPLICATION DATA:

APPLICATION NUMBER: 08

07/938,823 08/121,714 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di

Diskette, 1.44 Mb

Massachusetts

COMPUTER: IBW PS/2 Model 50Z or 55S OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1)

5.0)

SEQUENCE CHARACTERISTICS:
LENGTH: 390
TYPE: amino acid

STRANDEDNESS: TOPOLOGY: 11

linear

Sequence 6, Application US/08477112 Patent No. 5905023

GENERAL INFORMATION:

APPLICANT:

Sager, Ruth

TITLE OF INVENTION: MASPIN, TITLE OF INVENTION: TUMOR SUMBER OF SEQUENCES: 8

N, A NOVEL SERPIN WITH SUPPRESSING ACTIVITY

CITY: Boston

DRESSEE: Fish a NILL DRESSEE: 225 Franklin Street

Fish & Richardson P.C.

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,461
FILING DATE: Concurrently Herender:
CLASSIFICATION: 530
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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TELEFAX: (512) 474-757
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                      REFERENCE/DOCKET NUMBER: UM
ELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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NFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                             NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 EEIIMD 378
                                                                                                                                                                                                                                                                                                  CITY: Houston
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, Wh
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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. 5639726
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ISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             INVENTION: Peptide Mediated Enhancement Of INVENTION: Thrombolysis: Methods and Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fay, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ginsburg,
                                                                                                                                                                                                                                                                                                                                                                                                   Dell Paielli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lnsburg, David
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 390;
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US-08-840-204-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PACENTION Release #1.0, Version #1.30
CURRENT APPLICATION DATA: B208/948,997
FILING DATE: OCC-10-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATTORNEY/AGENT INFORMATTORN
                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 29; DB 3; Length 402; Best Local Similarity 100.0%; Pred. No. 38; Matches 6; Conservative 0; Mismatches 0; Indels
Sequence 2, Application US/08840204
Patent No. 6103498
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TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-315-461-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0%;
Matches 6; Conservative C
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TELECOMMUNICATION INFORMATION:
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APPLICANT: COLEMAN, T
APPLICANT: LAWRENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4: 402 amino acids
amino acid
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linear
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COLEMAN, TIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRAIN-ASSOCIATED INHIBITOR OF
TISSUE-TYPE PLASMINOGEN ACTIVATOR
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                        Gaps
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; TYPE: PRT
; ORGANISM: Bos
US-09-348-817A-4
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 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                        SEQ ID NO 4
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/348,817A CURRENT FILING DATE: 1999-07-08 PRIOR APPLICATION NUMBER: 08/948,997
                                                                                                                                                                                                                                                                                                                                                                                               09-348-817A-4
                                                                                                                                                                                                                                                                                                                                                                 equence 4, Application US/09348817A
atent No. 6191260
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                                                                                                                                                                                        RIOR FILING DATE: 1997-
RIOR APPLICATION NUMBER:
RIOR FILING DATE: 1996-
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TELEX: 90-4030 MRSNFOERSWSH
NFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        TLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
TLE OF INVENTION: Activator
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TELEPHONE: (202) 887-1500
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 EEIIMD 378
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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2000 PENNSYLVANIA AVENUE, NW
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 Score 29;
Pred. No.
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Pred. No.
38;
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US-08-796-899-29

; Sequence 29, Application US/08796899

; Patent No. 6160202
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                                                               ENERAL INFORMATION:
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Natent No. 6303338
                               APPLICANT:
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                                                                                                                                                           373 EETIMD 378
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APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                             ECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  ELEPHONE:
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6; Conserv
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APPLICATION DATA:
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                              BUSTOS, Mauricio M
CHERN, Maw-Shenq
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linear
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MODIFICATION OF SEED CROPS WITH TRANSCRIPTION FACTORS
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COUNTRY:

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Sequence 158, Appl
Patent No. 6159469
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Best Local Similarity
Matches 5; Conserv
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 836-203
NFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: MSDOS vo
SOFTWARE: ASCII Text
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APPLICATION NUMBER: US 08/319,544
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
STATE: Maryland
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TOPOLOGY: 11
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                         USA
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NO: 29:
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Pred. No. 2
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Best Local Similarity
""" As a file of the conserve of the conserv
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anit
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 0733
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-09-019-942-3
Sequence 3, Application US/09019942
Patent No. 6033855
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/019,942 FILING DATE: 06-FEB-1998 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & R!
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ZIP: 02110-2804
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TOPOLOGY: 11
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301) 309-8512
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heat shock protein grpE (heat shock protein b25.3) (hsp24) - Escherichia coli
heat shock protein grpE protein
R;Alternate names: grpE protein
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 24-Sep-1999
C;Accession: S01240; A55040
R;Lipinska, B; King, J; Ang, D.; Georgopoulos, C.
Nucleic Acids Res. 16, 7545-7563, 1988
A;Title: Sequence analysis and transcriptional regulation of the Escherichia coli grp
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Result No.

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ALIGNMENTS

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probable bHLH transcription factor [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear crees)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84616
                                                                                                                                                                                                                                                                                                                           plasminogen activator inhibitor type 1 precursor - C;Species: Mustela vison (American mink) C;Date: 19-0ct-1995 #sequence_revision 08-Feb-1996 C;Accession: JC4265
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C;Superfamily: heat shock protein grpE
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A;Residues: 1-197 <STO>
A;Cross-references: GB:AE005174; NID:g12517038; PIDN:AAG57724.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-400 <CHU>
A; Cross-references: EMBL: X58541; NID: g1164923; PID:
A; Experimental source: lung CCLG4 epithelial cells
C; Comment: This protein controls the activities of
                                                                                                                                                                                                                          R;Chuang, T.H.; Hamilton, R.T.; Nilsen-Hamilton, M. Gene 162, 303-308, 1995
A;Title: Cloning of the mink plasminogen activator A;Reference number: JC4265; MUID:98032362
A;Accession: JC4265
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.; Koo, H.; Moffat,
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Matches
Superfamily: antithrombin III
;Keywords: glycoprotein; plasminogen activator; serine proteinase inhibitor;
il-21/Domain: signal sequence *status predicted <SIG>
;22-400/Product: plasminogen activator inhibitor type 1 *status predicted <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: A84420;
Accession: E84616
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D; Nierman, W.C., ....
e 402, 761-768, 1999
cle: Sequence and analysis of chromosome 2 of
cle: Sequence A84420; MOID:20083487
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  A;Cross-references: GB:X04429; NID:g35271; PIDN:CAA28025.1; PID:g35272 R;Ginsburg, D.; Zeheb, R.; Yang, A.Y.; Rafferty, U.M.; Andreasen, P.A.
                                           A; Molecule type: mRNA
A; Residues: 1-402 < PAN>
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-9 <20N>
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 85-86;88-93;166-171;231-236;298-302;331-336;360-365;388-393 <FOL>
A; Residues: 85-86;88-93;166-171;231-236;298-302;331-336;360-365;388-393 <FOL>
A; Rocas-references: GB: M33136; NID: 9189543
A; Note: sequences of the intron/exon boundaries are shown
A; Note: sequences of the intron/exon boundaries are shown
A; Pannekoek, H; Veerman, H; Lambers, H; Diergaarde, P; Verweij, C.L.; van Zonneve
EMBO J. 5, 2539-2544, 1986
A; Title: Endotheilal plasminogen activator inhibitor (PAI): a new member of the serpi
A; Reference number: A91052; MUID: 87053819
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C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
C;Accession: A28107; S02551; A26996; I59126; JS0397; A25693; A26146; A29100;
C;Bosma, P.J.; van den Berg, E.A.; Koolstra, T.; Siemieniak, D.R.; Slightom,
J. Biol. Chem. 263, 9129-9141, 1988
A;Title: Human plasminogen activator inhibitor-1 gene. Promoter and structura
A;Reference number: A28107; MUID:88243790
A;Accession: A28107; MUID:88243790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:J03836; NID:g189579; PIDN:AAA60010.1; PID:g189580 R;F0110, M.; Ginsburg, D. Gene 84, 447-453, 1989
A;Title: Structure and expression of the human gene encoding plasminogen A;Reference number: JS0397; MUID:90128289
A;Accession: JS0397.
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R:Strandberg, L.; Lawrence, D.; Ny, T.
Eur. J. Biocham. 176, 609-616, 1988
A;Title: The organization of the human-plasminogen-activator-inhibitor-1 gene. Implic A;Reference number: S02551; MUID:89005111
A;Accession: S02551
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A; Residues: 1-14/"/,16-402 <STR>
A; Residues: 1-14/"/,16-402 <STR>
A; Residues: 1-14/"/,16-402 <STR>
A; Cross-references: EMBL:X13338; NID:g35244; PIDN:CAA31722.1; PID:g35245
A; Note: the complete translation is not annotated in GenBank entries HSPAI11, HSPAI12
A; Note: the complete translation is not annotated in GenBank entries HSPAI11, HSPAI12
R; LOSkutoff, D.J.; Linders, M.; Keljer, J.; Veerman, H.; van Heerikhuizen, H.; Pannek
B; Cochemistry 26, 3763-3768, 1987
B; Cochemistry 26, 3763-3768
B; Cochemistry 27, 3763-3768
B; Cochemistry 27, 3768
B; Cochemistry 27, 3
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N.Alternate names: plasminogen activator inhibitor, endothelial
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F;367/Inhibitory site: Arg (plasminogen activator) #status predicted
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A;Reference number: I59126; MUID:88289754
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A; Residues: 1-402 <LOS>
A; Residues: 1-402 <LOS>
A; Residues: 1-408, FR.
A; Residues: 1-408, FR.
A; Ross references: GB:M22321; GB:M17121; NID:g189576; PIDN:AAA60009.1; PID:g189578
A; Note: the sequence in GenBank entry HUWRAIRZ, release 109.0, (PID:g189578) has the R; Van Zonneveld, A.J.; Curriden, S.A.; Loskucoff, D.J.
R; van Zonneveld, A.J.; Curriden, S.A.; Loskucoff, D.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 5525-5529, 1988
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Pred. No.
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P.A.;

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Biochim. Biophys. Acta 1295, 103-109, 1996
A;Title: Characterization of the complex of plasminogen
A;Reference number: $70346; MUID:96283799
A;Accession: $70346
A;Status: preliminarry
A;Molor-1
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A;Residues: 364-402 <AND2>
A;Residues: 364-402 <AND2>
A;Cross·references: GB:X04731; NID:g35260; PIDN:CAA28442.1; PID:g35261
R;Laug, W.E.; Aebersold, R.; Jong, A.; Rideout, W.; Bergman, B.L.; Baker, J.
Thromb. Haemost. 61, 517-521, 1989
A;Title: Isolation of multiple types of plasminogen activator inhibitors from vascular A;Reference number: A60436; MUID:90020174
A;Recession: A60436
C;Superfamily: antithrombin III
C;Reywords: glycoprotein; serine proteinase inhibitor
F;1-23/pomain: signal sequence #status predicted <SIG>
F;24-402/Product: plasminogen activator inhibitor-1 #status experimental <WF;232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 370-375 <STO>
C; Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:UKHUT C; Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:UKHUT C; Comment: The concentrations of this protein have been associated with human throm C; Comment: Three types of PAI have been identified (see also PIR:A32853 and PIR:A39339). oma cells. Vascular endothelial cells may be the primary site of synthesis of plasma PAI C; Comment: Glycosylation is not required for inhibitory activity.
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A; Residues: 17-402 < WUN>
A; Residues: 17-402 < WUN>
A; Residues: 17-402 < WUN>
A; Rossire ferences: GB: X04744; NID: 935275; PIDN: CAA28444.1; PID: 9755747
A; Note: part of this sequence, including the amino end of the mature protein, was confired the part of this sequence, D.; Millan, J.L.; Loskutoff, D.J.
R; NY, T.; Sawdey, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 6776-6780, 1986
A; Title: Cloning and sequence of a cDNA cooding for the human beta-migrating endothelial-
A; Reference number: A25895; MUID: 86313660
                                                                                                                                                                          A;Gene: GDB:PAI1; PLANH1
A;Cross-references: GDB:120297; OMIM:173360
A;Map position: 7921 3-7922
A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1;
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Eur. J. Blochem. 241, 38-46, 1996
A;Title: Conformational changes of the reactive-centre
A;Reference number: S74133; MUID:97054589
A;Accession: S74133
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A; Residues: 225-235 <LAU>
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A; Title: cDNA cloning of human plasminogen activator-inhibitor from endothelial cells.
A; Reference number: A92766; MUID:87058123
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;Cross-references: GB:X04729; NID:g35263; PIDN:CAA28438.1; PID:g35264
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mbin III
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09, 1996
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A; Residues: 1-402 <MIM>
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Best Local
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6; Conserv
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plasminogen activator inhibitor-1 precursor - bovine N; Alternate names: endothelial-cell plasminogen activator inhibitor; PAI-1 C;Specles: Bos prinigenius taurus (cattle) C;Date: 28-Feb-1990 #sequence_revision 22-Apr-1995 #text_change 18-Jun-1999 C;Accession: S06745; A53855; S01324; S10906 R;Mimuro, J.; Sawdey, M.; Hattori, M.; Luskutoff, D.J.
hypothetical protein BB0205 - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000 C;Accession: E70125 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, I son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, I son, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Molecule type: protein
A;Residues: 24-49, L',51-63 <KAT>
C;Comment: Three types of PAI have been identified. PAI-1 is an acid-stable glycoprot
may be the primary site of synthesis of plasma PAI.
C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase,
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A; Residues: 153-235 (PEP>
A; Cross references: EMBL: X52906; NID: 9598; PIDN: CAA3709
A; Cross references: EMBL: X52906; NID: 9598; PIDN: CAA3709
R; Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.
Bur. J. Blochem. 176, 81-87, 1988
Bur. J. Blochem. 176, 81-87, 1988
A; Title: Bovine endothelial cell plasminogen activator
A; Reference number: S01324; MUID: 88329072
A; Accession: S01324
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R;Pepper, M.S.; Belin, D; Montesano, R.; Orci, L.; Vassalli,
J. Cell Biol. 111, 743-755, 1990
A;Title: Transforming growth factor-beta 1 modulates basic fi
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Nucleic Acids Res. 17, 8872, 1909
A;Title: cDNA for bovine type 1 plasminogen activator
A;Reference number: S06745; MUID:90067867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: glycoprotein; serine proteinase inhibitor F;1-23/Domain: signal sequence #status predicted <SIG> F;1-23/Domain: signal sequence #status predicted <SIG> F;24-402/Product: plasminogen activator inhibitor 1 #status predicted <MAT> F;232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicted F;369/Inhibitory site: Arg (plasminogen activator) #status predicted
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MUID:90338128
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Pred. No.
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A; Molecule type: DNA
A; Residues: 1-74 <WIL>
A; Cross-references: EMBL: ALO32644;
A; Experimental source: clone Y51H1A
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C; Superfamily: nodB homology
F; 113-264/Domain: nodB homology
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submitted to the EMBL Data Library, November 1994
*-Pearvintion: The sequence of S. cerevisiae cosmid L2142
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: E70125
A;Map position: 2
A;Introns: 22/1; 61/3; 372/2; 474/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y51H1A.6
                                                                                                                                                                                                submitted to the EMBL Data Library, October 1998
A; Reference number: 220309
A; Stetus: preliminary; translated from GB/EMBL/D
                                                                                                                                                                                                                                                                                                                               hypothetical protein Y51H1A.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A; Residues: 1-525 < KLE>
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                                                                    Gene: CESP:Y51H1A.6
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  polyhedrin - Galleria mellonella nuclear polyhedrosis virus (tentative seque RyAlternate names: inclusion body protein C; Species: Galleria mellonella nuclear polyhedrosis virus C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 31-Mar-2000 C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 31-Mar-2000 C;Accession: JN0407 R;Gusak, N.M.; Kozlov, E.A.; Ovander, M.N.; Serebryany, S.B. Bioorg, Khim. 7, 996-1007, 1981
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A; Residues: 1-120 <DEA>
A; Cross-references: EMB
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A; Residues: 1-120 < DAN>
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Best Local
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                                                                                                                                                                                                                                              41 DEIIMD
                                                                                                                                                                                                                                                                                        1 EEIIMD 6
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A;Description: electron transfer
C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Keywords: electron transfer; heme; iron; metalloprotein; transmembrane protein
F;2-77/Domain: cytochrome b5 core homology <CB5>
F;102-118/Domain: transmembrane #status predicted <TMM>
F;37,61/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-16, (0', 18-120 <TRU>
A;Residues: 1-16, (0', 18-120 <TRU>
A;Cross-references: EMBL:L22499; NID:g431761; PIDN:AAA67468.1; PID:g431762
A;Cross-references: EMBL:L2499; NID:g431761; PIDN:AAA67468.1; PID:g431762
A;Cross-reference in the control of the control o
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C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revisi
C;Accession: S63052; S47919; S67347
R;De Antoni, A.; D Angelo, M.; Dal I
submitted to the Protein Sequence D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Truan, G.; Eplnat, J.C.; Rougeulle, C.; Cullin, C.; Pompon, D. Gene 149, 123-127, 1994
A;Title: Cloning and characterization of a yeast cytochrome b(5)-encoding A;Reference number: $47919; MUID:95047457
A;Accession: $47919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:271387; NID:g1302031; PIDN:CAA95990.1; PID:g1302032; MIPS:YNA;Experimental source: strain S288C R;Truan, G; Epinat, J.C.; Rougeulle, C.; Cullin, C.; Pompon, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SGD:CYB5
A; Cross-references: SGD:S0005055; MIPS:YNL111c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z69382; NID:gl183941; PIDN:CAA93396.1; PID:gl183962
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Best Local Similarity 66.
Matches 4; Conservative
Similarity 83.1
5; Conservative
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es: protein N1949; protein YNL111
                                                      89.7%;
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Pred. No. 1.4e
2; Mismatches
                                                      Score 26; DB 2;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein YNL111c
          Mismatches
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1.4e+02;
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                                                                                                       Length 120
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sequence) (fra

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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights
A;Reference number: A75001
A;Accession: F75181
A;Starno.
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A;Accession: JN0407
A;Molecule type: protein
A;Residues: 1-240 <GUS2
A;Note: 18-Arg, 87-Ala, 87-Gly, 126-Met and 139-Glu were
C;Superfamily: nuclear polyhedrosis virus polyhedrin
C;Keywords: polyhedrin
                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 «KAW»
A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49533.1; PID:g54580.
A;Experimental source: strain Orsay
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Best Local Similarity
Thes 3; Conserve
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A;Molecule type: DNA
A;Residues: 1-274 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.; Ohfuku Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
A;Accession: D71032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30660.1; PID:g3257977
A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable autoantigen like protein - Pyrococcus horikoshii
C.Speciles: Pyrococcus horikoshii
C.Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C.Accession: D71032
                                                                                                                                                                                                                                                                                                                                                  polyribonucleotide nucleotidyltransferase related protein PAB0421 - Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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                                                    Superfamily: conserved
                                                                                                                                                                                                                                                                                                          ;Species: Pyrococcus abyssi
;Date: 20-Aug-1999 #sequence_revision
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Best Local Similarity
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                    hypothetical
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Pred. No.
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Pred. No. 1e+02;
2; Mismatches
Score
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26;
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DB
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274;
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                                                                      142 DEIIMD
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A;Molecule type: DNA
A;Residues: 1-284 <ARN>
A;Residues: 1-284 <ARN>
A;Cross-references: GB:AE001755; GB:AE000512; NID:g4981432; PIDN:AAD35997.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0916
C;Superfamily: Aeropyrum pernix hypothetical protein APE2212
                                                                                                                                                                                                                                                                                                                                             Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between
A;Reference number: A72200; MUID:99287316
A;Accession: C72320
                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thormotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72320
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ri
                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66. Matches 4; Conservative
139 DEIIMD 144
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213 EELVMD
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                                       1 EEIIMD 6
                                                                           Similarity 83...
5; Conservative
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                                                                                                89.7%;
83.3%;
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                                                                           Pred. No. 1.1e
1; Mismatches
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2; Mismatches
                                                                                                  1.1e+02
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RESULT 15
A70371
conserved hypothetical protein aq_814 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Jun-2000
C;Accession: A70371
C;Accession: A70371
R;Deckert, G; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70301; MUID:98196666
A;Recession: A70371
A;Recession: A70371
A;Accession: A70371
A;Readidues: 1-288 AA079
A;Crooss-references: GB:AE000708; NID:92983356; PIDN:AAC06959.1; PID:92983372; GB:AE00
A;Experimental source: Strain VF5
C;Gener: aq.814
C;Superfamily: Aeropyrum pernix hypothetical protein APE2212

Ouery Match 89.7%; Score 26; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps

2y 1 EEIIMD 6
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| 142 DEIIMD 147

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Search completed: March 18, 2002, 09:50:31

Job time: 240 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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    Query
Match
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7 escherichia
1 clostridium
9 african swi
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7 human herpe
6 bacillus po
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7 human musculu
5 streptococc
1 thermoplasm
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InterPro; IPR000740; GrpE.
Pfam; PF01025; GrpE; 1.
PRINTS; PR00773; GRPEPROTEIN.
PROSITE; PS01071; GRPE; 1.
Chaperone; Heat shock; 3D-structure; Complete proteome.
Chaperone; Heat shock; 3D-structure; Complete CRC64;
SEQUENCE 197 AA; 21798 MW; CDC4CD9D08AD4BEF CRC64;
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Harrison C.J., Hayer-Hartl M., di Liberto M.,
"Crystal Structure of the nucleotide exchange
the ATPase domain of the molecular chaperone D
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ECO2DBASE; B025.3; 6TH EDITION
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MEDITINE=96032362: PubMed=7557448:
Chuang T.H., Hamilton R.T., Nilsen-Hamilton M.;
Chuang T.H., Hamilton R.T., Nilsen-Hamilton M.;
"Cloning of the mink plasminogen activator inhibitor type-1 messeng-
RNA: an mRNA with a short half life.";
RNA: an mRNA with a short half life.";
Gene 162:303-308(1995)
-1- FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN
ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH
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nes 6; Conserv
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FUNCTION: STIMULATES, JOINTLY WITH DNAJ,
DNAK. HELDES TO RELEASE ADP FROM DNAK THUS
MORE EFFICIENTLY.
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1DKG; 20-AUG-97
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ia; Mustelidae; Mustela.
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e factor GrpE bound
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20-AUG-2001 (Rel. 40, Last annot
PLASMINOGEN ACTIVATOR INHIBITOR:
PLASMINOGEN ACTIVATOR INHIBITOR:
SERPINEL OR PAIL
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Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor;
SEQUENCE OF 153-235 FROM N.A.
TISSUE-Adrenal cortex;
MEDLINE-90338128; PubMed-1696269;
MEDLINE-90338128; PubMed-1696269;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Transforming growth factor-beta 1 modulates basic fibroblast growth factor-lnduced proteolytic and angiogenic properties of endothelial
                                                                                                                                                                                                                                                            SEQUENCE OF 24-63.
SEQUENCE OF 24-63.
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KATAGINE-88329072; PubMed-3262060;

KATAGINE K., Okada K., Hattori H., Ya
KATAGINE endothelial cell plasminogen
Purification and heat activation.";
Eur. J. Biochem. 176:81-87(1988).
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Bovidae; Bovinae; Bovidae; Bovidae; Bovidae; Bovinae; B
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MEDLINE-90067867; PubMed-2587231;
MIMURO J., Sawdey M., Hatiori M., Loskutoff D.J.;
Minuro J., Sawdey M., Hatiori M., Loskutoff D.J.;
"cDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).";
Nucleic Acids Res. 17:8872-8872(1989).
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Eukaryota; Metazoa;
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Best Loc
Matches
SEQUENCE FROM N.A.

MEDLINE-87053819; PubMed-2430793;

Pannekoek H., Veerman H., Lambers H., D.

van Zonneveld A.-J., van Mourik J.A.;

"Endothelial plasminogen activator inhil
the Serpin gene family."
EMBO J. 5:2539-2544(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X52906; CAA3709
PIR; S01324; S01324.
PIR; S06745; S06745.
HSSP; P01008; 1ATH.
                                                                                                                                                                                                             PAI1_HUMAN
P05121;
13-AUG-1987 (
13-AUG-1987 (
20-AUG-2001 (
PLASMINOGEN A
PLASMINOGEN A
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SEQUENCE
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ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
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J. Cell Biol. 111:743-755(1990).

ACTIVATOR, UROKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITH TPA MAY FUNCTION AS A MAJOR CONTOL POINT IN THE REGULATION OF FIBRINGUISIS.

J. CELLANEOUS: PAIL IS INACTIVATED BY PROTEOLYTIC ATTACK OF THE UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING THE J69(R)-370(M) BOND.

J69(R)-370(M) BOND.

J69(R)-370(M) BOND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                 HUMAN
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Glycoprotein;
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                                                                                                                                                                                Homo sapiens
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Local
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|73 EEIIMD
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SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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nilarity 100.0%;
Conservative 0.
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(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
ACTIVATOR INHIBITOR-1 PRECURSOR (PAI-1) (ENDOTHELIAL ACTIVATOR INHIBITOR) (PAI).
                                                                                                                                                                                                                                                                                                                                                                                                 378
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Primates;
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REACTIVE BOND.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
S-1 L (IN REF. 2).
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Pred. No.
                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae.
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                                      inhibitor
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                                                                   Diergaarde P.,
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12;
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                                                                   Verweij C.L.,
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SEQUENCE FROM N.A.
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Gene 84:447-453(1989).
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       X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=92114970; PubMed=1731226;
                                                                                                                                    SEQUENCE OF 17-402 FROM TISSUE-Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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Slightom J.L.;
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Ginsburg D., Zeheb R., Yang A.Y., Rafferty U.M., Andreasen P.A., Nielsen L., Dano K., Lebo R.V., Gelehrter T.D.; "cDNA cloning of human plasminogen activator-inhibitor from endothelial cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-87080762; PubMed-3025016;
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Nielsen L.S., Oppenhelmer C., Blasi F., Dance K.;
Plasminogen activator inhibitor type-1: reactive center
terminal heterogeneity determined by protein and cDNA seq
FEBS Lett. 209:213-218(1986).
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NY T., Sawdey M., Lawrence D., Millan J.L., Loskutoff D.J.;
"Cloning and sequence of a cDNA coding for the human beta-migrating
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MEDLINE-8900511; PubMed-3262512;

Strandberg L., Lawrence D., Ny T.;

"The organization of the human-plasminogen-activator-inhibitor-1

gene. Implications on the evolution of the serine-protease inhibitor
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TISSUE-Placenta;
MEDLINE-87105925; PubMed-3026837;
Wun T.C., Kretzmer K.K.;
"CONA cloning and expression in E. coli of inhibitor (PAI) related to a PAI produced length of the colin of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-47 AND 364-402 FROM N.A.
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13660; PubMed-3092219;
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263:9129-9141(1988).
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inders M., Keijer J., Veerman H.,
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en Berg E.A., Kooistra T.,
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                                                        plasminogen activator
Hep G2 hepatoma cell.";
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X-RAY CRYSTALLOGRAPHY (2.99 ANGSTROMS).
MEDLINE-99140119; PubMed-10368279;
Sharp A.M., Stein p.E., Pannu N.S., Carrell R.W.,
Sharp A.M., Stein p.E., Pannu N.S.,
Tarrell R.W.,
The active conformation of plasminogen activator
target for drugs to control fibrinolysis and cell
Structure 7:111-118(1999).
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Interfering with the inhibitory mechanism of structure of a complex formed between cleaved inhibitor type 1 and a reactive-centre loop pestructure 6:627-636(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      x-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
MEDLINE-98298439; PubMed-9634700;
Xue Y., Bjorquist P., Inghardt T., Linschoten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mottonen J., Strand A., Symer
Geoghegan K.F., Gerard R.D.,
"Structural basis of latency
Nature 355:270-273(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARÍANT THR-15.
MEDLINE-97337920; PubMed-9194591;
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                                                                                                                                                                                                                                                                                                                                                               FIBRINOLYSIS.

DISEASE: HIGH CONCENTRATIONS OF THIS PROTEIN HAVE
WITH HUMAN THROMBOEMBOLIC DISEASE.

MISCELLANEOUS: PAI1 IS INACTIVATED BY PROTEOLYTIC
UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), C
                                                                                                                                                                                                                                                                            MISCELLANEOUS: VASCULAR ENDOTHELIAL CELLS
OF SYNTHESIS OF PLASMA PAI.
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                       369(R)-370(M) BOND.

MISCELLANEOUS: TWO TYPES OF PAI HAVE BEEN IDENTIFIED. PAI-1 ACID-STABLE GLYCOPFOTEIN FOUND IN PLASMA AND PLATELETS AND I ENDOTHELIAL, HEPATOMA, AND FIBROSARCOWA CELLS.

MISCELLANEOUS: VASCULAR ENDOTHELIAL CELLS MAY BE THE PRIMARY
                                                                                                              X04429; CAA28025.1;

M14083; AAA60008.1;

X04729; CAA28438.1;

X04731; CAA28442.1;
                         X04729
X04731;
M16006;
M22321;
M22315;
M22316;
M22316;
M22317;
M22317;
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R.D., Goldsmith E.J.;
JOINED.
JOINED.
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tent is in
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EMBL
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Best Local S
Matches
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID=9823;
                                                                                                                                                                                                                        PAI1_PIG
P79335;
15-JUL-1998
15-JUL-1998
20-AUG-2001
PLASMINGGEN
                                                                               SEQUENCE FROM N.A.

MEDLINE=97206538; PubMed=9157595;
Bijnens A.P., Knockaert I., Cousin E
"Expression and characterization of
activator inhibitor-1.";
Thromb. Haemost. 77:350-356(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
Bijnens A.P., Knockaert I., Cousin E., Kruti
Thromb. Haemost. 77:1046-1046(1997).
-I- FUNCTION: THIS INHIBITOR ACTS AS "BAIT"
ACTIVATOR, UROKINASE, AND PROTEIN C. IT:
TPA MAY EUNCTION AS A MAJOR CONTROL POIL
FIBRINOLYSIS.
                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update
PLASMINGEN ACTIVATOR INHIBITOR-1 PRECURSOR
PLASMINGEN ACTIVATOR INHIBITOR) (PAI).
SERPINEL OR PAIL OR PLANHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serpin;
Glycopro
                                                               ERRATUM
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C X13340; CAB51737.1;
C X13341; CAB51607.1;
C X13342; CAB51607.1;
C X13343; CAB51738.1;
C X13344; CAB51739.1;
C X13345; CAB51729.1;
C X13345; CAA31729.1;
C X13346; CAA31208.1;
C X12764; AAA6007.1;
C X04744; CAA28444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A26996; ITHUP1.
S02551; S02551.
9PAI; 19-MAR-99.
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Similarity 100.0%;
6; Conservative (
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CAA31722.1; -
                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                     Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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ism; Signal;
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
A -> T.
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Pred. No. 12;
0; Mismatches
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             CONTROL POINT IN THE REGULATION
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3D-structure.
                                                                                                        :., Kruithof E.K.O.,
recombinant porcine
                                                                                                                                                                                                                                                                                402
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                                                     Kruithof E.K.O.,
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                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                      TISSUE PLASMINOGEN
PID INTERACTION WITH
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) (POTENTIAL).
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                                                                                                                                                                                                                            (ENDOTHELIAL
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Sus.
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plasminogen
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RESULT 6
CDA2_YEAST
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Matches
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01-NOV-1997 (Rel. 35
01-NOV-1997 (Rel. 35
CHITIN DEACETYLASE 2
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ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
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Q06702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a copyright of Bioinformatics and the EMBL the European Bioinformatics Institute There are the EMBL.
                                                                                                                          STRAIN-S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., D
Johnston M., Fulton L., Gattung S., Greco T., Kirsten J.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
Mardis E., Menezes S., Miller N., Valuely A., Pelus
Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
             reast 13:327-336(1997)
                                    MEDIINE-97279228; PubMed-9133736; Mishra C., Semino C.E., McCreath K.J., Specht C.A., Robbins P.W.; Cloning and expression of two chitin Saccharomyces cerevisiae.";
                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                       Saccharomycetales;
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NOV-1997 (Rel. 35, Last
NOV-1997 (Rel. 35, Last
TIN DEACETYLASE 2 PRECU
2 OR YLR307W OR L2142.2
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SIMILARITY: B
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UROKINASE-TYPE
 GLUCOSAMINE
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ilarity 100.0%;
Conservative
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WE RESIDUES
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370
232
288
352
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LONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                       Saccharomycetaceae;
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precursor (EC 3.5.1.41).
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THE N-ACETAMIDO IN CHITIN.
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N-LINKED (GLCNAC. . .) (PO'
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Pred. No.
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PLASMINOGEN ACTIVATOR INHIBITOR-1.
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Pred. No. 12;
Mismatches
                                                                                                                                                                                                                                                                                                                yeast)
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                                                  deacetylase
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                                                                                                                                                                                                                                                                                       Saccharomyces
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              GROUPS OF N-ACETYL-D
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                                                  genes
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RESULT
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Best Local S
Matches 5
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01-FEB-1995 (
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20-AUG-2001 )
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CARBOHYD
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                       MEDLINE-97745296; PubMed-9090005; de Antoni A., D Angelo M., Dal Pero F., Sartorello de Antoni A., Lanfranchi G., Valle G.; Pallavicini A., Lanfranchi G., Valle G.; The DNA sequence of cosmid 14-13b from chromosome the DNA sequence of cosmid 14-13b from chromosome the Company of the Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-FILIO;

MEDLINE-94237477; PubMed-8181746;

Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.;

Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.;

"Cloning and characterization of a yeast cytochrome b5-encoding

"Cloning and characterization of a yeast cytochrome b5-encoding

"Cloning and characterization of a yeast cytochrome b5-encoding

"Cloning and characterization of a yeast cytochrome b7-encoding

"Cloning and Characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEAST
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SGG); S0004299; CDA2.
InterPro; IPR002509; Polysac_deacet.
Pfam; PF01522; Polysac_deacet; 1.
Hydrolase; Chitin degradation; Signal;
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- I- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY DURING
- I- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    overlapping open reading frames."; Yeast 13:261-266(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                               FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. IT PLAYS A ROLE IN FATTY ACID DESATURATION AND IS INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
ZYMOSTEROL.
SUBCELLULAR
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EMBL; 269382; CAA93396.1; -.
EMBL; 271387; CAA95990.1; -.
PIR; S47919; S47919.
HSSP; P04166; 1B5M.
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01-NOV-1995
01-NOV-1997
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P42484;
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Electron
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                              Virology 208:249-278(1995).

-I: FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
-I: CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                           Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E.;
"Analysis of the complete nucleotide sequence of African swine fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African swine fever virus (strain BA71V) (ASFV).
Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
African swine fever-like viruses.
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pfam; FP00173; heme_1; 1.
prints; pr00363; cytoCHROMEB5.
pr0SITE; pS00191; CYTOCHROME_B5_1; 1.
pr0SITE; pS50255; CYTOCHROME_B5_2; 1.
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BELONGS TO THE CYTCCHROME B5 FAMILY.
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32, Last sequence update)
35, Last annotation updat
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61 HEME LIGAND
118 POTENTIAL,
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HEME LIGAND (BY SIMILARITY).
POTENTIAL.
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598EF2A6730CAD19 CRC64;
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01-NOV-1997
20-AUG-2001
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MILL C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Stott J.L., Geoghagen N.S.M., Peterson J.D., Sadow P.M., Hanna M.C.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Noese C.R., Venter J.C.;

*Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR01725; RNA_polK_14KD.
Pfam; PF01192; RNA_polK; 1.
PROSITE; PS01111; RNA_POLK, 14KD; 1.
Transferase; DNA-directed RNA polymerase; Transcription.
SEQUENCE 147 AA; 16691 MW; 6D0B66D77025CD45 CRC64;
                                                                                                                                     Hypothetical protein; Transmembrane; Complete proteomer TRANSMEM 17 37 POTENTIAL. SEQUENCE 292 AA; 33508 MW; B8A34C29B3A51246 CRC64;
                                                                                                                                                                                                              TIGR; MJ1495; -.
                                                                                                                                                                                 InterPro; IPR002825; DUF114. Pfam; PF01972; DUF114; 1.
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-I- SIMILARITY: STRONG, TO M.JANNASCHII MJ0137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence jannaschii.";
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Methanococcus.
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20 STRAIN=RD / KW20 / ATCC 51907;

21 X MEDLINE=95350630; PubMed=7542800;

22 X MEDLINE=95350630; PubMed=7542800;

23 Fleischmann R.D. Adams M.D. White O., Clayton R.A., Kirkness E.F.,

24 Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

25 Kerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

26 Kerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

27 Kerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Kelley J.M.,

28 Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

29 Weldman J.F., Phillips C.A., Spriggs T., Hebblom E., Cotton M.D.,

20 Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

29 Kine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

20 Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

20 Venter J.C.;

20 Whole-genome random sequencing and assembly of Haemophilus

21 Influenzae Rd.";
                                                                                                                                                                                                                               30-MAY-2000 (I
30-MAY-2000 (I
20-AUG-2001 (I
HYPOTHETICAL 7
D2013.9
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01-NOV-1995 (Rel. 3
20-AUG-2001 (Rel. 4
MU-LIKE PROPHAGE FI
                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematc
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Mortimore B., Matt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete SEQUENCE 508 AA; 57190 MW;
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Science 269:496-512(1995).
-1- SIMILARITY: STRONG, TO PHAGE MU PROTEIN GP28.
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5; Conservative
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Proteobacteria;
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
L 76.7 KDA PROTEIN D2013.9 IN CHROMOSOME
      Matthews
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Last annotation upon protein GP28.
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5BFC6833E2F1242B CRC64;
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RESULT 12
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EMBL; 247809; CAA87778.1; -
EMBL; 247809; CAA87783.1; -
EMBL; 247809; CAA87783.1; -
EMBL; 247808; CAA87783.1; -
EMBL; 247808; CAA87783.1; -
EMBL; 247808; CEA1535.
InterPro; IPRO01214; SET; -
PROSITE; PS50280; SET; 1.
Hypothetical protein.
SEQUENCE 662 AA; 76750 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
01-NOV-1997
20-AUG-2001
                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentitles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-868087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Clayton R.A., Gocayne J.D.,

Scutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1998) to the EMBL/GenBank/DDBJ
-- SIMILARITY: CONTAINS 1 SET DOMAIN.
-- SIMILARITY: STRONG, TO HUMAN KIAA0153.
            EMBL; U67539; AAB98963.1; TIGR; MJ0961; -.
                                                                                                                                                                                                                Science
                                                                                                                                                                                                                           "Complete genome sequence jannaschii.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii.
Archaea; Euryarchaeota; M
Methanococcus.
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Q58371;
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5; Conserv
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273:1058-1073(1996).
ILARITY: BELONGS TO THE MCM FAMILY.
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662 AA; 76750 MW;
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L MCM-TYPE
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, Last annotation of the protein MJ0961.
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Pred. No. 1.1e+02;
1; Mismatches (
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IPR001208; MCM.

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RESULT 13
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P46837; P76689;
01-NOV-1995 (Rel.:
15-JUL-1999 (Rel.:
20-AUG-2001 (Rel.:
                                                                                                                                                                                                                                                                                                                                                                                                       (1)
SEQUENCE FROM N.A.
STRAIN-K12 / M01655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode M.A., Rose D.J.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                              IDENTIFICATION BY MASS SPECTROMETRY.

MEDLINE-99420866; PubMed-10493123;
Fountoulakis M, Takacs M.-F., Berndt P., Langer
"Enrichment of low abundance proteins of Escher:
hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
-1- SIMILARITY: STRONG, TO H.INFULENZAE HIO568.
-1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
                                                                                                         EMBL; U18997; AAA58204.1; ALT_FRAME. EMBL; U18997; AAA58205.1; ALT_FRAME. EMBL; AE000416; AAC76432.1; ALT_INITHSSP; P05055; 15RO.
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long, as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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PROSITE; PS50051; MCM_2;

Hypothetical protein; Transcription regulation; DNA-binding;

DNA replication; Cell cycle; ATP-binding; Complete proteome.

DOMAIN 34 542

MCM.

NP_BIND 384 391

ATP (POTENTIAL).

SEQUENCE 762 AA; 87526 MW; 3323509057464C12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
Bacteria; Proteobacteria;
                                     RNA-binding;
                                                    ECOGene; EG12932; yhgf.
InterPro; IPR003029; S1.
Pfam; PF00575; S1; 1.
SMART; SM00316; S1; 1.
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SMART; SM00350
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Complete proteome.
651 720 S1 MOTIF.
754 755 QP -> HA
73 AA; 85119 MW; EA54D9E
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-> HA (IN REF. 1; AAA58205).
EA54D9ED952A8229 CRC64;
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1.3e+02;
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                                                                                      RPB6_ASFM2
Q08399;
Q1-OCT-1994
Q1-OCT-1994
Q1-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
CHEMICAL-DAMAGING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Azeddoug H., Reysset G.;

*Cloning and sequencing of a chromosomal fragment from Clostridium acetobutylicum strain ABKn8 conferring chemical damaging agents and UV resistance to E. coll recA strains. ";

*Curr. Microbiol. 29:229-235(1994).

-I- FUNCTION: NOT KNOWN; COULD CONFER METHYL METHANE SULFONATE (MM: MITOMYCIN C (MC), AND UV RESISTANCE.

-I- SIMILARITY: BELONGS TO THE CAPAB / TERDEXZ FAMILY.
                                                                                                                                                                                                                                                                                                                        InterPro;
Pfam; PFO
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDRB_CLOAB
Q45811;
African swine fever virus (isolate Malawi Lil 20/1) (ASFV).
Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
African swine fever-like viruses.
NCBI_TaxID=10500;
[1]
                                                                                                                                                     ASFM2
                                                                PMWK-CL.
                                                                            DNA-DIRECTED
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Pro; IPR003325; TerD.
PF02342; TerD; 1.
NCE 139 AA; 15429 MW;
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30, Last sequence update)
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POLYMERASE, SUBUNIT 6 HOMOLOG
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38, Last sequence update)
38, Last annotation update)
AGENT RESISTANCE PROTEIN B.
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83.3%;
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Pred. No. 1.3e
1; Mismatches
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Pred. No. 35;
1; Mismatches
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RX MEDLINE-93324382; PubMed-8332503;
RA MEDLINE-93324382; PubMed-8332503;
RA LU Z., Kutish G.F., Sussman M.D., Rock D.L.;
RT An African swine fever virus gene with a similarity to eukaryotic RT RNA polymerase subunit 6."
RNA POLYMERASE SUBUNIT FAILUR.
CC 1- FUNCTION. DNA JETENBURT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA LITTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
CC 1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE + C. CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE + C. CATALYTIC BELONGS TO THE ARCHAEBACTERIA RPOK / EUKARYOTIC RPB6 C. RNA POLYMERASE SUBUNIT FAMILY.
CC 1- SIMILLARITY: BELONGS TO THE ARCHAEBACTERIA RPOK / EUKARYOTIC RPB6 C. RNA POLYMERASE SUBUNIT FAMILY.
CC 1- SIMILLARITY: BELONGS TO THE ARCHAEBACTERIA RPOK / EUKARYOTIC RPB6 C. This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation to the European Boinformatics Institute. There are no restrictions on its conditions on the Swiss Institute. There are no restrictions on tway modified and this statement is not removed. Usage by and for commercial conditions and the EMBL outstation of the EMBL outstation
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O9uz50 pyrococcus
O9hr2 halobacteri
O27747 methanobact
O21692 lactococcus
O44714 caenorhabdi

Opfid2 uncultured
Opwxp5 thermotoga
Opwxp5 thermotoga
Opyxp5 thermotoga
Opfid2 streptomyce
Opwx10 sulfolobus
Opefz3 lactococcus
Opfid2 brachydanio
Opwym5 thermotoga

O9v5n5 drosophila O9m9g4 arabidopsis O9vj73 drosophila O9ngp1 dictyosteli O9n533 caenorhabdi

homo sapien arabidopsis phaseolus v

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sp_unclassified:*
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Q9xw3 caenorhabdi
Q91113 arabidopsis
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Q9y2y0 homo sapien
Q9d385 mus musculu
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Q9hhbl methanococc
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082397;
01-NOV-1998 (TIEMBLITE). 08, Created)
01-NOV-1998 (TIEMBLITE). 08, Last sequence update)
01-JUN-2001 (TIEMBLITE). 17, Last annotation update)
HYPOTHETICAL 32.6 KDA PROTEIN.
O51223 PRELIMINARY;
O51223;
O1-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.R., Venter J.C.;
Shen M., Ronning C. M., Fraser C.M., Somerville C.R., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AC005617, AAC63587.1;
EMBLF, AC005617, ARC63587.1;
InterPro; IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudloctyledons; core eudlcots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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01-MAR-2001
01-MAR-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R. Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Ha van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J. Utterback T., Watthey L., McDonald D., Artiach P., Bowman G. Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatsmith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:580-586(1997).
EMBL; AE001131; AAC56601.1; -.
TIGR; BB0205; -.
                                                                                                                Submitted (OCT-1999) to the EMBL/GenBank/DDBJ database EMBL; AF197899; AAG28517.1; -
Interpro; IPRO02316; trNA-synt.pro.
PRINTS; PRO1046; TRNASYNTHPRO.
Aminoacyl-trNA synthetase; Ligase.
SEQUENCE 460 AA; 53292 MW; DAB364435B808E44 CRC64;
                                                                                                                                                                                            "A single class II synthetase specifies two translation.";
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Stathopoulos C., Li T.,
                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROLYL-TRNA SYNTHETASE (EC 6.1.1.15).
Methanococcus maripaludis.
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STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
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                                                                                                                                                                                                                        Ibba M., Soll D.;
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                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae
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                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rochaetales;
                                                             96.6%;
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                                                                                                                                                                                                                                   Longman R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease spirochete).
Spirochaetaceae; Borrelia
                                                 Score 28; DB Pred. No. 2.1e 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 2;
Pred. No. 1.4e+02;
Mismatches 0;
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837F0B2A35EB255D CRC64;
                                                                                                                                                                                                                                     Vothknecht U.C., Becker
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                                              7.1e+02;
0;
                                                                           DB 1;
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ion update)
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                                                                                                                                                                                   databases
                                                                          Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 525;
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lickey E.K., Gwinn M.,
lrdson D.,
                                                    Indels
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Best Local S
Matches 4
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09A256;
01-JUN-2001
01-JUN-2001
01-JUN-2001
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Milerman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vannathevan J., Ermolaeva M., White (
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL, AE006028; AAK25672.1; -.
TIGR, CC3710; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FLU5;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
MEDLINE-98290546; PubMed-9628582;
Sato S., Kaneko T., Kotani H., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TEMBLIEL. 16, Created)
01-MAR-2001 (TEMBLIEL. 16, Last sequence update)
01-UN-2001 (TEMBLIEL. 17, Last annotation update)
GENOMIC DNA, CHROMOSOME 5, TAC CLONE:K18P6.
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                                                                          EMBL; AB010068; BAB11210.1; -.
Interpro; IPR001934; HMA.
Interpro; IPR001230; Prenyltn.
Pfam; PF00403; HMA; 2.
                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thallana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned pl and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caulobacter crescentus
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        PS00294;
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120 AA; 12483 MW; B30E9BCA06F9283A CRC64;
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        prenyLation; UNKNOWN_1.
; 35350 MW; 5A97CA58833BCDE0 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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86;
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Query Match Best Local S Matches 4

Similarity 4; Conser

Conservative

Pred. No. 2.4e 2; Mismatches

4e+02

DB 10;

Length 319; Indels

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ID 09LJL3 PKELLILI.

AC 09LJL3;

PT 01-0CT-2000 (TrEMBLrel. 15, Last sequence update)

PT 01-0CT-2000 (TrEMBLrel. 15, Last annotation update)

PT 01-0CT-2000 (TrEMBLrel. 15, Last sequence update)

PT 01
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Best Local Similarity 66.7
Matches 4; Conservative
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Frevello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Latreille P.,
Lightning J., Lloyd C., Memurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Riften L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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PROSITE; PS50157; ZINC_FINGER_C2H2_2;
DNA_binding; Zinc_finger_
SEQUENCE 574 AA; 65776 MW; 9146676
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InterPro; IPR000822; Znf-C2H2.
Pfam; PF00096; Zf-C2H2; 1.
SMART; SM00355; ZnF_C2H2; 1.
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NCBI_TaxID=6239;
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9 (TrEMBLrel. 12,
1 (TrEMBLrel. 17,
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66.7%;
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4.6e+02;
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RA Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Barownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Kontsuki S.,
RA Havashizaki Y.,
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Query Match
Best Local Similarity
Matches 5; Conserv
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Q9CQW6;
Q1-JUN-2001 (TIEMBLEEL 17,
Q1-JUN-2001 (TIEMBLEEL 17,
Q1-JUN-2001 (TIEMBLEEL 17,
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DNA Res. 7:217-221(2000).
EMBL; AP000419; BAB02957.1;
                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:665-690(2001).
EMBL; AK006646; BAB24686.1; -.
EMBL; AK0066418; BAB24578.1; -.
MGD; MGI:191433; 1700027H16Rik.
SEQUENCE 152 AA; 17571 MW; 4DE5F01744ED1E58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COLUMBIA;
Kaneko T., Kato T.,
Submitted (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TremBLrel
1700027H16RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; Metalloprotease.
SEQUENCE 1052 AA; 117654 MW;
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PubMed-10907853;
                                                                                                                                                                                                                                                                                                                                                 layashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1700027H16RIK.
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                                      89.7%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
          Score 26; DB 11;
Pred. No. 1.9e+02;
1; Mismatches 0;
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Pred. No. 8.7e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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NA KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush G.,
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A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush G.,
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A Schriml L.M., Staubli F., Suzuki R., Tomita M., Washio T.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Bustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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Q9D385;
01-JUN-2001
01-JUN-2001
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09Y2YO;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TREMBLREL. 17, Last annotation update)
ARF-LIKE 2 BINDING PROTEIN BART1 (BINDER OF ARL TWO).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-MEDULLA O
MEDLINE-21085660; PubMed-11217851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLRel. 17, Last snotation update)
01-JUN-2001 (TIEMBLRel. 17, Last snotation update)
6330544B05RIK PROTEIN (SIMILAR TO BINDER OF ARL TWO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001) to the EMBL; AF126062; AAD20633.1; EMBL; BC003087; AAH03087.1; SEQUENCE 163 AA; 18822 MF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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"The Arf-like 2 (Ari2) binding protein BART1: purification, cloning, and initial characterization.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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29 EDIIMD 34
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
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Pred. No.
1; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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2.1e+02;
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Similarity 66. 4; Conservative

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
RA Hyons F., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Kawaji H., Kohtsuki S.,
RA Hayashtawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA col
Nature 409:685-690(2001).
EMBL; AKO06511; BAB24026.1; -
MGD; MGI1916746; 1700023M23Rik.
SEQUENCE 175 AA; 20552 MW; 15AEB6A38F87706E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
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"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
1700029M23RIK PROTEIN.
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Score 26; DB 11;
Pred. No. 2.2e+02;
2; Mismatches 0;
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Q9F0U6;
Q9F0U6;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                 TISSUE-BONE MARROW:
Zhao M., Gu J., Li N., Peng Y., Han Z., Chen Z.;
A novel gene expressed in human bone marrow.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF217515; AAF67626.1;
SEQUENCE 204 AA; 24053 MM; 39E4E5F78E020260 CRC64;
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Mammalia; Eutheria;
NCBI_TaxID-9606;
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"Isolation of a cathepsin b-like sequence from adult Ancylostoma
ceylanicum.";
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01-OCT-2000 (TrEMBLTel. 15,
01-OCT-2000 (TrEMBLTel. 15,
UNCHARACTERIZED BONE MARROW
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae;
NCBI_TaxID=53326;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CATHEPSIN B-LIKE PRECURSOR PROTEIN (FRAGMENT).
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180 AA;
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180
20099 MW; · F3729B7CC683E601
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Ancylostoma
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Best Local Similarity 83.7
Matches 5; Conservative
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"Sequence of o-chlorophenol reductive dehalogenase from
"Sequence of o-chlorophenol reductive dehalogenase from
Desulfitchbacterium chlororespirans CO23.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF204275; AAG43484.1;

Interpro; IPR000595; CMMP_binding.

Interpro; IPR001808; HTH_CRP.

SMART; SM00100; cMMP; 1.

SMART; SM00419; HTH_CRP; 1.

SMART; SM00419; HTH_CRP; 1.
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01-JUN-2001 (TEMBLEel. 17, Last annotation update)
HYPOTHETICAL 26.9 KDA PROTEIN.
Desulfitobacterium chlororespirans.
Bacteria, Firmicutes; Bacillus/Clostridium group;
Hellobacterium group; Desulfitobacterium.
NCBL_TaxID-51616;
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98344137; PubMed-9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Takamiya M., Ohfuku Y.
Sakai M., Oqura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res S. 55.757(1961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-OT3;
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Archaea; Euryarchaeota;
NCBI_TaxID=53953;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last snootation update)
274AA LONG HYPOTHETICAL AUTOANTIGEN LIKE PROTEIN.
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01-AUG-1998 (TrEMBLrel.
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Pfam; PF01138; RNase_PH; 1.
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213 EELVMD
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3e+02;
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Search completed: March 18, 2002, 09:51:57 Job time: 286 sec

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Result
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Perfect score:
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                                                                                                                                                                                                                                                            Score
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29
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Gapop 10.0 , Gapext 0.5
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AAR07245
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AAW98747
AAW98747
AAU03391
AAG85015
AAY72392
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Peptide used to re PAI-1 (E350->R). H PAI-1 (E47350) mu H. pylori GHPO 103 Pyrenophora teres Shrimp white spot Corn LHT1 encoded Polypeptide encode Amino acid sequenc Neisseria meningit
                                                                                                                                                                                                                                                            Description
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AAY69860	AAY69859	AAY69858	AAY69857	AAY69856	AAY69855	AAB78402	AAB78399	AAB78395	AAB78394	AAB78388	AAB78387	AAB78386	AAY90001	AAY89998	AAY89994	AAY89993	AAY89987	AAY89986	AAY89985	AAB92200	AAY42738	AAY01812	AAB23601	AAW99302	AAB79355	AAG92728	AAB69050	AAB93497	AAY84439	AAY81763	AAB08637	AAY86073	41	
FIV gp36 envelope	FIV gp36 envelope	gp36	gp36	gp36 e	gp36	e pol	e pol	e pol:	e pol	e pol	pol	Core polypeptide T	Core polypeptide f	e pol	Core polypeptide f	Core polypeptide f	pol	pol	Core polypeptide f	Thrombin inhibitor		Peptide used to re		Human BAI3 protein	Corynebacterium gl	4	Human ribonucleoti	Human protein segu	Amino acid sequenc	Streptococcus pneu	Amino acid sequenc	 S. pneumoniae deri 	enas	

ALIGNMENTS

RESULT AAY01813

29-JUN-1999

(first entry)

AAY01813;

AAY01813 standard; peptide; 6 AA

Peptide used to regulate scuPA.

AWA Abnormal cell migration; PAI-1-dependent cell adhesion; scuPA clearance KW pathological cell migration; angiogenesis; organogenesis; ovulation; KW inflammation; cancer; tumor cell invasion; metastasis; atherosclerosis. XX Synthetic.
XX Synthetic.
XX W09920295-A1.
XX W09920295-A1.
XX PN W09920295-A1.
XX 17-OCT-1999.
XX 17-OCT-1998; 98WO-US21800.
XX PF 15-OCT-1997; 97US-0062274.
XX (UYPE-) UNIV PENNSYLVANIA.
XX PI Cines D, Higazi AA;
XX PI Cines D, Higazi AA;
XX PP Peptide composition
XX Peptide composition
XX Example 1; Page 31; 63pp; English.

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AAR07245
The sequence represents AAs 1-380 of the PAI-1 protein chain. To The mutant was obtd. by site directed mutagenesis of the wild type gene. It has an Arg at posn. 350 replacing the Glu residue which is thought to form a contact with the t-PA Arg residue at posn. 304. The binding is modelled on that of the complex formed between trypsin and BPI where the Ty-39 of trypsin forms a Van der Waal's contact with Ile19 of BPI. In the mutant the Glu residue has been replaced by and Arg residue, restoring the electrostatic interaction that was disrupted by the construction of the Arg304-> Complementary to the mutant t-PA. The mutant serpin mutant is therefore active inhibtor than its parent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                Serine protease mutant of the chymotrypsin super-family - compsn. including it and genes encoding it, resistant to inhibition by PAI-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sambrook JF,
Gerard RD;
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06-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue plasminogen activator; light chain; mutant; serine protease; chymotrypsin; salt bridge; serpin; inhibitor; t-PA.
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                                                                                                                                                                                                                                                                                                                                                 Claim 34; Page 60; 75pp;
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nilarity 100.
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89US-0319212
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Best Local S
Matches 6
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative (
                                                                       This PAI-1 mutant has Glu 350 of wild-type mature PAI-1 substituted by Arg. This substitution was chosen to selectively alter the negatively-charged Glu residue to a positively-charged Arg residue and promote potential interactions with the negatively charged Glu 304 residue in the PAI-1-resistant tPA mutant tPA(Glu304) (see AAR23804). The mutant tPAI-1 showed an increased rate constant of interaction with tPA(Glu304) c.f. wild-type PAI-1. The sequence given as AAR23813 does not appear in the specification but has been compiled from the known PAI-1 sequence (see WO9013648) and the description given in the specification.
                                                                                                                                                                                                                              New zymogen plasminogen activator mutants - inhibition by cognate serpin inhibitors in for myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue plasminogen activator; mutant; serine protease; zymogen-like; PAI-1; plasminogen activator inhibitor; coagulation; chymotrypsin superfamily.
                                                      Sequence
                                                                                                                                                                                                          Example 2; Page 55; 82pp; English.
                                                                                                                                                                                                                                                                           WPI; 1992-150888/18
                                                                                                                                                                                                                                                                                                  Gerard RD,
                                                                                                                                                                                                                                                                                                                                             28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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Similarity 100.0%;
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                                                      402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350) mutant
                                                                                                                                                                                                                                                                                               Gething MH,
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/label= mature_PAI-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        leader
                                                                                                                                                                                                                                                                                                  Goldsmith EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402
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Score 29; DE
Pred. No. 43;
0; Mismatches
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Pred. No. 41;
0; Mismatches
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         DB 43;
                                                                                                                                                                                                                                                                                                  Madison
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    resistant
plasma and

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                      13;
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                                                                                                                                                                                                                                                                                                  EĽ,
                      Length
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                                                                                                                                                                                                                                                                                                   Sambrook JF;
                                                                                                                                                                                                                                          to
platelets,
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                      402;
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RESULT
AAW98747
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                                                                   RESULT
                                                                                                                                     Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1997;
01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                         This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used forthe production of antibodies.
           12-SEP-2001
                              AAU03391;
                                                                                                                                                                                                                                                                                          Claim 8; Page 1594-1596; 2054pp; English
                                                                                                                                                                                                                                                                                                          New isolated Helicobacter polynucleotides for the diagnosis, prevention and treatment infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-542293/46.
N-PSDB; AAX14466.
                                                                                                                                                                                                                                                                                                                                                                                 Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9843478-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H. pylori GHPO 1033 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW98747;
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                                                AAU03391 standard;
                                                                                                1 REIIMD 6
|||:||
270 reilmd 275
                                                                                                                                                                                       Sequence
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                                                                                                                                       Local Similarity
nes 5; Conserv
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                                                                                                                                        Conservative
          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0902615.
97US-0833457.
97US-0881227.
                                                                                                                                                                                         Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US06371
                                                  Protein;
                                                                                                                                                 93.1%;
                                                  758
                                                                                                                                                 Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 Miller C,
                                                  ₽
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                                                                                                                                         Mismatches
                                                                                                                                       DB 19; I
1.1e+02;
ches 0;
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                                                                                                                                                                                                                                                                                                                       used to develop products of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                  ₽P,
                                                                                                                                                           Length 340;
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AAG85015
ID AAG8
XX
AC AAG8
XX
DT 11-9
XX
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            11-SEP-2001
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Query Match
Best Local S
Matches 4
                                                                                                                                                                                          The sequence represents Pyrenophora teres partial peptide synthetase, CPS1 CPS1 is an enzyme thought to be involved in the production of peptide toxins, which are involved in the pathogenic infection of corn crops. The nucleic acids and proteins can be used as targets for anti-fungal compounds to prevent fungal corn infection and the nucleic acids can be used in gene therapy to alter the biosynthetic pathway for the peptide toxins to lower the pathogenicity of the fungi.
                                                                                                                                                                                                                                                                           Claim 24; Page 39; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPS1; peptide synthetase; peptide toxin; fungal pathogen; corn crop infection.
                    AAG85015;
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200138489-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrenophora teres.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrenophora teres partial CPS1 peptide synthetase
                                                                                                                                                                                                                                                                                            New isolated nucleic acid molecule from a plant pathogen useful preventing plant pathogenic infections -
                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                        Yoder OC,
                                                                                                                                                                                                                                                                                                                                                                         (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-2000;
                                      AAG85015 standard;
                                                                                      328 revvmd
                                                                                                       1 REIIMD 6
                                                                                                                                                                                                                                                                                                                           2001-367672/38.
DB; AAS06685.
                                                                                                                         h 93.1%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                       Turgeon
                                                                                                                                                                            758 AA;
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(first entry)
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524..543
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424..435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Peptide synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "J
217..225
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755..70
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221..2
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                                                                                                                                                                                                                                                                                                                                                        ВС,
                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Peptide synthetase motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Peptide synthetase motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Peptide synthetase motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cyclization domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Peptide synthetase
                                                                                                                                                                                                                                                                                                                                                        F
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                                       1245
                                                                                                                            Score 27; DB
Pred. No. 2.5e
2; Mismatches
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                                       B
                                                                                                                            DB 22; I
2.5e+02;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             motif,
                                                                                                                                             Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    core
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                                                                                                                             Gaps
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RESULT
AAY7239
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                      26-DEC-2000
                                                         US6165792-A.
                                                                                                                              Corn; lysine- and histidine-specific transporter;
proline transporter; transgenic plant; immunologic
                                                                                                                                                                                   Corn LHT1 encoded by cDNA clone ctaln.pk0048.h2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                           Zea mays.
                                                                                                                                                                                                                         24-APR-2001
                                                                                                                                                                                                                                                              AAY72392;
                                                                                                                                                                                                                                                                                             AAY72392 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Figure 3; 626pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-355877/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu X, Yang F, He J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2000; 2000WO-US28888
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                                                                                                                                                                                                                                                                                                                                                                                        792 relimd 797
                                                                                                                                                                                                                                                                                                                                                                                                                           1 REIIMD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             white
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 83.:
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH62795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1245 AA;
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spot Bacilliform virus (WSBV) protein 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99CN-0124717.
                                                                                                                                                                                                                                                                                               Protein; 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pham
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB
Pred. No. 4.1e
1; Mismatches
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                                                                                                                              ransporter; LHT1;
immunological screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1e+02;
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RESULT
AAR83032
ID AAR8
XX AAR8
AC AAR8
AC AAR8
AC CAP
KW CAP
KW CAP
KW SErc
XX STr
YX YOS
PN WOS!
PN WOS!
PF 16-1
PR 16-
PR 16-
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The invention relates to lysine and histidine-specific transporter CC (LITH), proline transporter and their corresponding cDNA clones. It is useful for producing transgenic plants with altered expression level of camino acid transporters, in cell types or developmental stages in which corresponding transporters, and the obtained transgenic plants of they are not normally found, such that the obtained transgenic plants companies to salt and water stress. The level of lysine, in its invention is also used for constructing a chimeric gene encoding all corresponding to the amino acid transporter, where in the expression of chimeric gene results in the production of altered levels of amino acid transporter in a transformed host cell. Synthetic peptides obtained from the corresponding transporter are used for immunising animals to produce polyclonal or monoclonal antibodies, which facilitates the immunological excreening of cDNA expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                      Capsular polysaccharide; cps; peptide; flanking region; detection; serotype; diagnosis; prevention; Streptococcus pneumoniae.
(UABR-) UAB RES FOUND
                                                                        16-MAY-1995;
                                                                                                             23-NOV-1995
                                                                                                                                                  WO9531548-A1
                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                             Polypeptide encoded by 5' flanking region of cps gene
                                                                                                                                                                                                                                                                                                                     03-APR-1996
                                                                                                                                                                                                                                                                                                                                                        AAR83032;
                                                                                                                                                                                                                                                                                                                                                                                         AAR83032 standard; peptide; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is corn lysine and histidine specific transporter (LHT1) from clone ctaln.pk0048.h2, isolated from a corn tissue ctaln CDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding amino acid transporters, e.g. lysine- and histidine-specific transporter and proline transporter, useful for transgenic plant production with altered expression level of the amino acid transporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-090485/10.
N-PSDB; AAD02471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-1999;
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| 246 rqiimd
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les 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                   pneumoniae
                                       94US-0243546
                                                                          95WO-US06119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB
Pred. No. 1.4e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Le.
, 1.4e+02;
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                infection; bacterial capsule; serotype specific; virulence; diagnosis; capsule synthesis; cassette model; binary model; cassetting-in; flanking region; non-serotype specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus pneumoniae capsular polysaccharide genes for detection, serotyping and for diagnosis and prevention pneumoniae infection
                                                                                                                                                                                                                                            02-JUN-1997;
16-MAY-1994;
                                                                                                                                                                                                                                                                                       02-JUN-1997;
                                                                                                                                                                                                                                                                                                                 07-SEP-1999
                                                                                                                                                                                                                                                                                                                                             US5948900-A
                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of Cps3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY33889 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 166; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillard JP,
                                                                            Non-serotype-specific flanking nucleotide sequences derived from Streptococcus pneumoniae capsular polysaccharide genes, useful as hybridization probes for identifying serotype-specific capsular polysaccharide genes
                                                                                                                                                WPI; 1999-517979/43.
N-PSDB; AAZ11798.
                                                                                                                                                                                        Dillard J, Yother J;
                                                     Claim
Serotype-specific cps genes encode the
                          This is is the amino acid sequence of the capsule synthesis
                                                                                                                                                                                                                (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 REIIMD 6
|:||||
52 rkiimd 57
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DB; AAT05485.
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                    6a; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                       pneumoniae.
                                                                                                                                                                                                                                              97US-0867030.
94US-0243546.
                                                                                                                                                                                                                                                                                       97US-0867030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25;
Pred. No.
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 various enzymatic
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                             protein
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RESULT 10
AAY755
XX AAY755
XX 21-MAR
DE Neisse
XW Neisse
XW Neisse
XW antiba
XW antiba
XW ANTiba
XX ANTIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC functions of capsule synthesis and hence determine the particular CC structure of the capsule polysaccharides produced. Therefore cps genes CC determine the serotype of the virus.

CC AR211799, AR211800, AR211801 and AR211802) may be used in hybridization CC aR211799, AR211800, AR211801 and AR211802) may be used in hybridization CC assays to identify the location of DNA flanking serotype-specific cps CC deditionally, the flanking regions are involved in recombination CC and integration of the type specific cps genes during virus CC and integration of the type specific cps genes during virus CC excrype-specific cps genes) is integrated between the nucleic acids CC of the flanking region, the resulting construct can be stably integrated CC miss allows the locus of the serotype-specific can be stably integrated CC isolated and characterized. The cps gene sequences may then be used as CC hybridization probes to identify and quantify specific serotypes of S. CC pneumoniae or to recombinantly produce the gene products for use as axis control of the municipal control of the serotypes of S. CC antigens in immunization protocols.
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Best Local
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                        Fraser C,
Petersen J
Tettelin F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis ORF 747 protein sequence SEQ ID NO:2558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY75542 standard;
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                             WPI; 2000-062150/05
N-PSDB; AAZ54304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
(GENO-) INST GENOMIC RES.
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52 rkiimd
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                                                                                                        Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
, Venter JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                    98US-0083758.
98US-0094869.
98US-00998994.
98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB Pred. No. 53; 1; Mismatches
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                                                                                                                                        Hickey
Ratti
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                                                                                                                                        Masignani V,
Scalato E,
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Scarselli
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for

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Query Match
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Matches 4; Conserv
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31-JUL-1998;
02-SEP-1998;
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09-OCT-1998;
09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAX54537 to AAX54576 and AAZ54616 to AAZ54373 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                          Fraser C, Galeotti C, Grandi G, Petersen J, Pizza M, Rappuoli R, Tettelin H, Venter JC;
WPI; 2000-062150/05
N-PSDB; AAZ54305.
                                                                                                                                                                                                                                                                                                      30-APR-1999;
                                                                                                                                                                                                                                                                                                                                    11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                  W09957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY75543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY75543 standard; Protein; 102
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                                                                                                                                                                                                                          02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis ORF 747 protein sequence SEQ ID NO:2560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 1216; 1453pp; English.
                                                                                                           (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
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68 reivld 73
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98US-0094869
98US-0098994
98US-0099062
98US-0103794
98US-0103794
98US-0103796
99US-0121528
                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy
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                                                           Hickey E,
Ratti G,
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                                                          Masignani V,
Scalato E,
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                                                             Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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              Sequence
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Novel Neisserial polypeptides predicted

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useful antigens

Query Match

86 . 29 ;

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Query Match
Best Local
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                               The amino acid sequence is that 6 which was translated from DNA AAR21409-R21413 and AAR20056.
                                                                                                                                          New DNA sequences which act assaying DNA sample from reinfected with P carinii
                                                                                                      Claim 3; Fig 3; 42pp; English
                                                                                                                                                                                                                N-PSDB; AAQ20065.
                                                                                                                                                                                                                                                                                                                                       01-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADH dehydrogenase 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1992
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                                                                                                                                                                                                                                WPI; 1992-007487/01.
                                                                                                                                                                                                                                                                  Wakefield AE,
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                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS
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68 reivld 73
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assay; AIDS;
174 AA;
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Pred. No. 95;
2; Mismatches
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                                                   of P. carinii NADH dehydrogenase from plasmid pAZ112. See also
                                                                                                                                                                                                                                                                    ER;
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RESULT 14
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Best Local Similarity
Taches 4; Conservi
                                                                                                                                                                                                               This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AA796173-296494) and their encoded proteins (see C Polynucleotides (see DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to expression or activity of interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of infection, dysfunction and disease.
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 551-552; 640pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae proteins and screening compounds for antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-159452/14.
N-PSDB; AAZ96394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Black MT,
Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-1996;
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antimicrobial; antibiotic; pathogenesis; infection.
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                                                                                                                  Conservative
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1; Mismatches 0;
                                                                                                                  Score 25; DB Pred. No. 2e+C 2; Mismatches
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2e+02;
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Best Local S
Matches 4
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                                                       Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS; bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism; kidney disease; diabetes; fimunosuppressive disorder; otitis media; pneumococcal septicaemia; sinusitis; meningitis; therapy.
                                                                                                                               Streptococcus pneumoniae protein sequence ID119.
                                                                                                                                                              02-JUN-2000
                                                                                                                                                                                         AAY81763;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a polypeptide of the thymidylate kinase family (tdk polypeptides), and is derived from Streptococcus pneumoniae. Tdk polynucleotides may be used to recombinantly produce the tdk polypeptides either in vivo (e.g. as part of a genetic vaccination procedure) or in vitro (e.g. as part of a fermentation culture). The nucleic acids and proteins may be used to diagnose diseases in which the tdk polypeptides are expressed, such as infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 3; 41pp; English.
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N-PSDB; AAA64398.
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 WO200006738-A2
                             Streptococcus pneumoniae
                                                                                                                                                                                                                     AAY81763 standard;
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arren PV;
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2e+02;
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This sequence represents a Streptococcus pneumoniae protein of the CC invention. The proteins (or their homologues, derivatives and/or invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunogens or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or city of the detection or diagnostic of S. pneumoniae infection, by contacting a sample to be tested with them. Agents capable of antagonising, inhibiting or interfering with the city of the function or expression of the protein or polypeptide are useful in medical compositions in the treatment or prophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions young children, the elderly, and in patients with predisposing conditions or with immunosuppressive disporders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otilis media, sinusitis, and
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcal proteins and polynucleotides useful for diagnosis, treatment and prophylaxis of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-195301/17.
N-PSDB; AAZ91859.
                                       meningitis.
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19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Le Page RWF, Wells JM, Hanniffy SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIAL TECHNICS LTD.
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212 AA;
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99US-0125329.
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Ouery Match 86.2%; Score 25; DB 21; Length 212; Best Local Similarity 66.7%; Pred. No. 2ë+02; Matches 4; Conservative 2; Mismatches 0; Indels

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Search completed: March 18, 2002, 09:48:56 Job time: 365 sec

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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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29
1 REIIMD 6
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
/cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
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US-09-258-258-23
US-08-40-204-3
US-08-40-204-3
US-08-121-714-6
US-08-131-461-7
US-08-131-461-7
US-08-141-7008-8
US-09-09-383-16
US-08-325-547-3
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 7, Appli
8, Appli
8, Appli
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; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 60/097,222
; EARLIER FILING DATE: August 20, 1998
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Zea mays
US-09-370-253-4
                                                                                                                                                                                                                                                                      RESULT 2
US-08-867-030B-7
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                                                                                               Sequence 7, Application US/08867030B
Patent No. 5948900
GENERAL INFORMATION:
APPLICANT: Yother et al.
TITLE OF INVENTION: Streptococcus pneumoniae
TITLE OF INVENTION: Capsular Polysaccharide Genes
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Allen, Stephen M.
APPLICANT: Sakai, Hajime
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
FILE REFERENCE: BB-1200
                                            STREET: BULL
STREET: BULL
CITY: Houston
STATE: TX
STATE: TX
USA
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STATE: TX
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
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246 RQIIMD 25
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US-08-766-738-3

US-08-766-738-3

US-08-578-709-13

US-08-560-098A-55

PCT-US96-03916-61

PCT-US96-03916-71

US-08-336-031-2

US-08-302-853-7

PCT-US95-06725-2

US-08-902-853-7

PCT-US95-06725-2

US-08-961-083-158

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; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
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GENERAL INFORMATION:
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Matches 5; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/243,546 FILING DATE: May 16, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,030B
FILING DATE: June 2, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/243,546
APPLICATION NUMBER: 08/243,546
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,546
FILING DATE: 16-MAY-1994
                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06119
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 REIIMD 6
|:||||
52 RKIIMD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (713) 777-2321
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                               FILING DATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                             SOFTWARE: Paten
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                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                          DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                         E OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benjamin Aaron Adler, Ph.D., J.D. TRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                           Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                       Application PC/TUS9506119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                         E: Arnold, White & Durkee P.O. Box 4433
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                                                                                                                                                                                                                                                          United States of America
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Pred. No.
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    Mismatches

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17;
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                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 212
; TYPE: PRT
; ORGANIZM: Streptococcus pneumoniae
US-09-259 109-2
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US-09-259-109-2
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/259,109
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                  equence 6, Applicati
atent No. 5792749
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Burnham, Martin K. R. APPLICANT: Zalacain, Magdalena APPLICANT: Biswas, Sanjoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Traini, Christopher M.
APPLICANT: Warren, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chalker, Alison F.
APPLICANT: Ingraham, Karen A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
     CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS, WHITHAM & MCGINN
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 REIIMD 6
|:|||
52 RKIIMD 57
                                                                      JUMBER OF SEQUENCES:
                                                                                   ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (713 TELEX: 79-092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Parker, David L. 32,165
                                                                                                                                                                                                                                                   51 REVILD 56
                                                                                                                                                                                                                                                                1 REIIMD 6
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                                                                                                                                                                   Application US/08781020
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linear
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                                                                                                                      Wright, H. Tonie
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                                                                                   METHOD AND COMPOSITION FOR LOWERING LOW DENSITY LIPOPROTEIN CHOLESTEROL
                                                                                                                                                                                                                                                                                                                             86.2%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                 Score 25; DB 4; Pred. No. 67; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                 Length 212;
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0; Gaps

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

USA

20191

Reston VA

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Query Match
Best Local Similarity
"atches 5; Conserva
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RESULT .7
US-08-565-386-23
                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-038-935-6
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                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/038,935
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 08/781,020
EARLIER FILING DATE: 1997-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wright, H. Ton
APPLICANT: Janciauskiene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW DENSITY (TILE OF INVENTION: LIPOPROTEIN CHOLESTEROL LE REFERRNCE: 29022Da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: VC:
LECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Whitham, Michael E. REGISTRATION NUMBER: 32,635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 EIIMD 9
                                                                                  2 EIIMD 6
                                                                5 EIIMD 9
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    Application US/09038935
    6150332

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                                                                                                                               Conservative
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                                                                                                                                               82.8%; Score 24; DB 4; Length 33; 100.0%; Pred. No. 16;
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                                                                                                                                 Mismatches
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                                                                                                                                 0; Indels
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                                                                                                                                 Gaps
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SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: not releval
DOPOLOGY: linear
MIRCULE TYPE: peptide
US-08-565-386-23
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BACTÉRIOPHAGE OF CHLAMYDIA PSITTACI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                     CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              APPLICANT: Renault, Pierre TITLE OF INVENTION: Nucleic TITLE OF INVENTION: synthas NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 20
PELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
TELEFAX: (716) 263-1487
                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
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REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 176/60040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/565,386
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                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                               Godon, Jean-Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716-263-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bavoil, Patrik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
                                                                                                                                                                                                                                                                                                                                      Nucleic acid coding for an alpha-acetolactate synthase from Lactococcus and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Stanislav
                                                                                                                                                                                US/08/403,866
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Pred. No.
                                                            20747/30
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 3, Application US/08840204
tent No. 6103498
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 978450 (WUT)
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 REIAMD 167
351 EIIMD 355
                                                                                                                                                                                                                                                                              ELECOMMUNICATION INFORMATION:
                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                        Local Similarity es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 REIIMD 6
                            2 EIIMD 6
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/840,204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DECULE TYPE: PIC
                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGANISM: Lactococcus lactis subsp. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LICANT: STEFANSSON, STEINGRINGR P.
E OF INVENTION: MUTAUT PLASMINOGEN ACTIVATOR-INHIBITOR
E OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                       379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAWRENCE, DANIEL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORRISON & FOERSER
                                                                                                                                                                                                                                                                   (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENNSYLVANIA AVENUE, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                           single
                                                                                                                                                                                                                                     MRSNFOERSWSH
                                                                                                                                                                                                                                                               887-1500
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                                                                      82.8%;
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                  Length 379;
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                                                        Indels
                                                        0; Gaps
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US-08-650-275-3
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                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
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                                                                                                                                                                                                         Sequence 3, Application US/09181318 Patent No. 6001632
                                                                                                                                                                                                                                       -09-181-318-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                            ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1086627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/6: FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                  313 REFVMD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
                                          COUNTRY:
                                                                        CITY: Palo Alto
                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                             1 REIIMD 6
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LECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                        ADDRESSEE:
                                                                                                                                    TLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE ABER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 389 amino acids amino acid
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                                                                                     3174 Porter Drive
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                                            U.S.
                                                                                                                                                            Murry, Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415-852-0195
                                                                                                                                                                             Braxton, Scott Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murry, Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braxton, Scott Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                        Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN PROTEIN DISULFIDE ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                        82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,954
                                                                                                                                                                                                                                                                                                                                                                         Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0067 US
                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 389;
                                                                                                                                                                                                                                                                                                                                                            Indels
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Query Match 82.
Best Local Similarity 66.
Matches 4; Conservative
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                                                      FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/
FILING DATE: 09/01/97
APPLICATION NUMBER: 07/
APPLICATION NUMBER: 07/
APPLICATION NUMBER: 07/
FILING DATE: 02/28/91
FILING DATE: 02/28/91
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LENGTH: 389 amino acid
                                                                                                                                                                                                                                              SOFTWARE: WordPerfect
CURRENT APPLICATION DATA
                                      FILING DATE: 02/28/91 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1086627
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/121,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE OF INVENTION: MASPIN, A NOVEL SERPIN WITH LE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
CANT: Sager, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 amino acids
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                                                                                                                                                   07/938,823
                                                                         07/662,216
                                                                                                             07/844,296
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Pred. No. 2.2e+0
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Best Local Similarity 100.
"Arches 5; Conservative
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/121
APPLICATION NUMBER: 07/938
APPLICATION NUMBER: 07/938
APPLICATION NUMBER: 07/844
APPLICATION NUMBER: 07/844
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 580100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULT 13
-08-477-108A-6
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                                                                                               TELEFAX: (617) 542-89
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
                                                                                                                                       REFERENCE/DOCKET NUMBER: 06570/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/477,108A FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02110-2804
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                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 Franklin Street
                                                                                                                                   (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anisowicz,
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SYSTEM: MS-DOS (Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
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08-121-714-6

STREET: 225 | CITY: Boston

313 REFVMD 318

1 REIIMD 6

ELEPHONE:

0; Gaps

US-08-477-108A-6

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; STRANDEDNESS: ; TOPOLOGY: 11 US-08-477-112-6
RESULT
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Best Local Similarity
Watches 5; Conserva
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US-08-477-112-6
                                                                                   Query Match
Best Local Similarity luv.
"arches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121;714
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quence 6, Application US/08477112
tent No. 5905023
ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WOODDERECT (Version 5.1)
CURRENT APPLICATION MINUS
                                           2 EIIMD 6
|||||
374 EIIMD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EIIMD 6
|||||
374 EIIMD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" D1
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
STREET:
STREET:
Massar
15
                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E OF INVENTION: MASPIN, A NOVEL SERPIN WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                           (617) 542-8906
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Search completed: March 18, 2002, 09:49:41
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Best Local Similarity
Vatches 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: 07/938
APPLICATION NUMBER: 07/938
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662
                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDERFIELD AND SOFTWARE: WORDERFECT (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 34,819
TELECOMMUNICATION INFORMATION:
TELEPHONE: /617 670
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                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
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REGISTRATION NUMBER:
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225 Franklin Street
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Maximum DB
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2: pir2:*
3: pir3:*
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Match
BLOSUM62
Gapop 10.0 , Gapext 0.5
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C;Species: Methanococcus jannaschii
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ALIGNMENTS

C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: C64364
R;Bult, C.J.; White, O; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Black, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Sadow, P.M.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woes A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woes A;Itle: Complete genome sequence of the methanogenic archaeon, Methanococcus janna: A;Accession: C64364
A;Accession: C64364 A;Experimental source: strain Bristol N2; C;Genetics: A;Gene: CESP:C17E7.8 A;Map Position: 5 A;Introns: 27/3; 64/1; 164/3; 242/3; 326/1 submitted to the EMBL Data Library, July 1997
A; Description: The sequence of C. elegans cosmid C17E7
A; Reference number: 221091
A; Accession: T31823 hypothetical protein C17E7.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #text_change C;Date: 29-Oct-1999 #text_change C;Accession: T31823
R;Bradshaw, H. A;Map position: REV458767-457625 C;Superfamily: NADH dehydrogenase (ubiquinone) 49K protein A; Status: preliminary; translated A; Molecule type: DNA A; Residues: 1-413 GBRA> A; Cross-references: EMBL: AF016443; A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-380 <BUL> A;Cross-references: GB:U67501; GB:L77117; NID:g2826289; Query Match Best Local S Matches 6 Genetics: 133 REIIMD 138 1 REIIMD 6 Similarity 6; Conserv Conservative EMBL:AF016443; PIDN:AAC24282.1; GSPDB:GN00023; CESP:C17E7.8 se: strain Bristol N2; clone C17E7 100.0%; 0 from Score 29; Pred. No. Mismatches GB/EMBL/DDBJ DB 16; 2 <u>.</u> Length 380; Indels PIDN: AAB98504.1; PID:g15912: 29-Oct-1999 0 Gaps 0

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C;Accession: F86742
R;Bolotin, A.; Wincker, P.; Mar
Genome Res. in press, 2001
A;Title: The complete genome sr
A;Reference number: A86625
A;Accession: F86742
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Best Local Similarity
Watches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                            ribonuclease [imported] - Lactococcus lactis subsp. lactis (strain II1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Aquifex aeolicus
Date: 08-May-1998 #sequence_revision
Accession: B70482
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Best Local
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                                                                                                                                                                                                                   Molecule type: DNA residues: 1-817 <570>
Cross-references: GB:AE005176; NID:g12723878; Experimental source: strain II1403
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Best Local
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Residues: 1-456 <AQF>
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371 REVIMD 376
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Pred. No. 18;
0; Mismatches
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69;
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Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, kl. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reev J. Bacteriol 179, 7135-7155, 1997
A.Title: Complete genome sequence of Mothers Transfer Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.; Ohfuku, Y.; Funahashi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence
                                                                                                                                                                                                       conserved hypothetical protein MTH545 - Methanobacterium thermoautotrophicum C;Species: Methanobacterium, thermoautotrophicum C;Datc: 05-Dec-1997 *sequence_revision C;Datc: 05-Dec-1997 *sequence_revision C;Datc: 05-Dec-1997 *Sequence_revision C;Datcession: A69172 C;Accession: A69172 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-340 <TON>
A;Residues: 1-340 <TON>
A;Cross-references: GB:AE000647; GB:AE000511; NID:g2314645; PIDN:AAD08509.1; PID:g23
C;Superfamily: branched-chain-amino-acid transaminase BAT1
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A; Residues: 1-243 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Pyrococcus
C; Date: 14-Aug-1998 #9
C; Accession: G71209
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
A69172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; A;Title: The complete genome sequence of the gastric pathogen Helicobacter pyl A;Reference number: A64520; MUID:97394467
A;Accession: D64703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete sequence and gene organization of the genome of a hyper-thermophil:
A;Reference number: A71000; MUID:98344137
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son, J.D.; Kelley, J.M.
Nature 388, 539-547, 19
A; Authors: Wallin, E.;
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999
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270 REILMD 27
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les 5; Conserv
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.; Funahashi, T.;
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genome sequence of Methanobacterium thermoautotrophicum r: A69000; MUID:98037514
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Tanaka, T.; Kudoh, Y.; Yame
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: Pred. No. 46;
1; Mismatches
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Pred. No.
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Yamazaki,
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                                                                                                                                                                                        J.; Aldredge,
son, R.; Jiwani
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hypothetical protein YPL004c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein LPAl3c; hypothetical protein YP8132.09c
c;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 12-Dec-1997
C;Accession: S52527; S59689
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C;Accession: B71661
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Fitle: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Fitle: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Fitle: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Fitle: The genome sequence not shown; translation not shown A;Status: preliminary nucleic acid sequence not shown; translation not shown
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C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 *sequence_revision 21-Nov-1998 *text_change 03-Nov-2000
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Best Local Similarity
Watches 5; Conserv
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A; Residues: 1-341 <HAL>
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Best Local Similarity 83.:
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: strain AB972;Experimental source: strain AB972;Experimental source: strain AB972;Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Waubmitted to the EMBL Data Library, August 1995;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ubmitted to the EMBL Data Library, February 1995; Reference number: S52519; Accession: S52527
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Experimental source: strain Madrid E
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Residues: 1-327 <AND>
ell division protein fts2 [imported] - Buchnera sp. (strain APS);Species: Buchnera sp.;Species: Buchnera sp.;Sate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
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Residues: 1-341 <BAD>
Cross-references: EMBL:248483; NID:9683777; PID:9683786; MIPS:YPL004c
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248 RQIIMD 253
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320 REIILD 325

Search completed: March 18, 2002, Job time: 241 sec

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A;Gene: fts2; BU212
C;Superfamily: cell division protein fts2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A;Reference number: A84930; MUID:20445173
A;Accession: A84955
                                                                                                                                                                                                                                                                                                  J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus. A;Reference number: Z22020; MUID:99281911
A;Accession: T41879
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule tune: num
                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T41879
R;Gomi, S.; Majima, K.; Maeda,
J. Gen. Virol. 80, 1323-1337, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACMNPV orf142 - Bombyx mori nuclear polyhedrosis virus (isolate T3) C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV C;Species: Joolate T3 A;Variety: Isolate T3 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
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A; Residues: 1-384 <STO>
A; Cross-references: GB:AP000398; GSPDB:GN00144
A; Experimental source: strain APS
              Ş
                                                                                                                                                                A;Note: Orf_118
C;Superfamily: Orgyia pseudotsugata nuclear polyhedrosis virus hypothetical protein 1
                                                                                                                                                                                                                      A;Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63808.1; PID:g3745961
A;Experimental source: isolate T3
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-476 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity bb..
Conservative
                                                      Query Match 89.7%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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1 REIIMD 6
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; Pred. No. 95;
2; Mismatches
                                                                                  Score 26; DB 2;
Pred. No. 1.2e+0
                                                               Mismatches
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type; DNA A;Residues: 1-437 kMTH>
A;Cross-references: GB;AE000837; GB;AE000666; NID:g2621613; PIDN:AAB85051.1; PID:g262167
A;Experimental source: strain Deita H
C;Genetics:
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C;Superfamily: glucose-6-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: MTH545
                                                                                                                                                                                                                          NA polymerase III, epsilon chain (dnaQ) RP732 - Rickettsia prowazekii
;Species: Rickettsia prowazekii
;Coate: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
;Accession: A7163
;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T
ature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lucose-6-phosphate 1-dehydrogenase - Deinococcus radiodurans (strain
;Species: Deinococcus radiodurans
;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: B75377
White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, M.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.
Best Local Similarity 66.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:AE002003; GB:AE000513; NID:g6459358; PIDN:AAF11158.1; PID:g645938
Experimental source: strain R1
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Matches 5; Conserv
                                                                                                                                                                      Title: The genome sequence of Rickettsia Reference number: A71630; MUID:99039499 Accession: A71633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
Molecule type: DNA
Residues: 1-590 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lence 286, 1571-1577, 1999
Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans Reference number: A75250; MUID:20036896
Accession: B75377
                                                                                                                                                     Status: preliminary; nucleic acid sequence
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                                                                                                                type: DNA
1-229 <AND>
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A; Molecule type: protein
A; Residues: 1-64,'X',66,'X',68-69 <MO2>
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                R;Moriyama, R.; Makino, S.
Arch. Blochem. Blophys. 256, 606-617, 1987
A;Title: Interaction of glyceraldehyde-3-phosphate dehydrogenase f band 3 polypeptide.
A;Reference number: A61591; MUID:87297550
A;Accession: A61591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            band 3 anion transport protein - bovine (fragments) C;Species: Bos primigenius taurus (cattle) C;Date: 21-Nov-1993 #sequence_revision 28-Apr-1995 C;Accession: S05658; A61591
                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Moriyama, R.; Kawamatsu, S.; Kondo, Y.; Tomida, M.; Makino, S. Arch. Biochem. Biophys. 274, 130-137, 1999
A;Title: Antigenic determinants of the cytoplasmic domain of band 3 from bovine eryt. A;Reference number: S05658; MUID:89372925
                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-306 < MOR>
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Best Local Similarity 83.3
Matches 5; Conservative
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Pred. No. 53;
1; Mismatches
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RESULT 11
A71681
A71681
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Adecession: A71681
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmarl Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria A;Reference number: A71680; MUID:99039499
A;Accession: A71681

A;Accession: A71681
A;Accession: A71681
A;Accession: A71681
A;Accession: A71681
A;Accession: Translation not shown
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-236 (AND)
A;Cross-references: GB;AJ235271; GB;AJ235269; NID:g3868717; PIDN:CAA14723.1; PID:g386

A;Cross-references: GB:AJ235271; GB:AJ235269; A;Experimental source: strain Madrid E C;Genetics:

A;Gene: pdhA; RP261 C;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate

Query Match 89.7%; Score 26: DB 2; Length 326: Best Local Similarity 83.3%; Pred. No. 79; Matches 5; Conservative 1; Mismatches 0; Indels 1 REIIMD 6

277 REIILD

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RESULT
HEMN_A(
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XX MEDLINE-98196666; PubMed-9537320;

XA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

XA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,

XA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;

YET THE COMPLETE GENOME Of the hyperthermophilic bacterium Aquifex

YET A EQUITES ANAEROBIC TRANSFORMATION OF COPROPORPHYRINOGEN-III INTO

YET COPROTION: REQUITES MAGNESIUM, AND NAD (OR NADP) FOR ACTIVITY.

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_AQUAE
                                                                                                            EMBL; AE000774; AAC07846.1; -.
InterPro; IPR003401; Coprogen_an_ox.
Pfam; PF02473; Coprogen_an_ox; 1.
Porphyrin blosynthesis; Oxidoreductase; Magnesium; NAD; Complete proteome.
SEQUENCE 456 AA; 53785 MW; 4E494103B8EF6342 CRC64;
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Bacteria; Aquificales;
NCBI_TaxID=63363;
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ILVC_LACLA
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                                                Score 28; DB 1; Pred. No. 19; 1; Mismatches
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rhizobium m

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D73G_RICPR
ODPA_RICPR
CDPA_RICPR
F7SZ_BUCAI
RUD2_RHIME
Y142_NPVAC
NIFU_BACVU
PSAF_HORVU
THIL_PYRHO
T376_AQUAE
FYV1_HUMAN
EF2_HALHA
MA_EMENI

941 1522 1986 1296 123 1155 178 178 206 270 299 299 309

YIIK_BPCHP
CYB5_YEAST
CYB5_YEAST
C59A_MOUSE
RL13_AERPE
RL13_ACFPE
RL5_ARCFU
GRPE_ECOLI
KTHY_DEIRA
FPC_ZYMMO
YE95_METJM
BAH_STRHY
MARE_CHICK
P2A_BRANA
NOD3_RHIME
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P2A4_ARATH
P2A4_MEDSA

deinococcus
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9 streptomyce
0 gallus gall
brassica na
0 rhizobium m
0 arabidopsis
8 arabidopsis
9 medicago sa

RESULT

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Minimum Maximum

DB

length: 0 length: 2000000000 of

hits satisfying chosen parameters:

100059

100059 segs, 36664B27 residues

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score:

Sequence:

US-09-544-665-4 29 1 REIIMD 6 3

protein

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protein search, using sw model

Copyright

GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd

March 18, 2002, 09:52:26;

Search time 24.53 Seconds (without alignments) 8.968 Million cell updates/sec

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RESULT 3
TBG_NEUCR
ID TBG_N
AC P5337
DT 01-OC
DT 01-OC
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15-JUL-1998 (Rel. 36,
20-AUG-2001 (Rel. 40,
BRANCHED-CHAIN AMINO &
ILVE OR HP1468.
TBG_NEUCR
P53377;
01-OCT-1996
01-OCT-1996
20-AUG-2001
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MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.
Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
MCKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.
Cotton M.D., Weldman J.M., Fujil C., Bowman C., Watthey L., Wallin
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000647; AAD08509.1; -. HSSP; P00510; 1A3G. TIGR; HP1468; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBE outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=210;
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Local
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PATHWAY: VALINE AND ISOLEUCINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT
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5; Conserv
(Rel. 34, Created)
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                                                                                             STANDARD;
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. 36, Last sequence 40, Last annotations.
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subdivision; Helicobacter group;
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(C. STRAIN-MADRID E;

(C. STRAIN-MADRID E)

(C. STRAIN-MADRID E)

(A. Andersson S.G.E., Zomorodipour A., Andersson J.O.,

(A. Andersson S.G.E., Zomorodipour A., Andersson J.O.,

(A. Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,

(A. Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,

(A. Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,

(A. Sicheritz-Ponten J., Winland C.G.;

(The genome sequence of Rickettsia prowazekii and the origin of

(The genome sequence of Rickettsia prowazekii and the origin of

(The genome sequence of Rickettsia prowazekii and the origin of

(The University Of The Republicative Synthesis IN BACTERIA.

(C. -I-FUNCTION SUBUNIT CONTAIN THE EDITING FUNCTION AND IS A

(C. THE EPSILON SUBUNIT CONTAIN THE EDITING FUNCTION AND IS A

(C. PROOFREADING 3'-5' EXONUCLEASE (BY SIMILARITY).
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Matches 4
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InterPro; IPR003008; Tubulin_FtsZ.
Pfam; PF00091; tubulin; 1.
PRINTS; PR01161; TUBULIN.
PRINTS; PR01164; GAMMATUBULIN.
PROSITE; PS00127; TUBULIN; 1.
Microcubules; GTP-binding.
GTB (DC)
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DP3E_RICPR STANDARD; PRT; 2
OP3CJ9;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2001 (Rel. 40, Last annotation
DNA POLYMERASE III, EPSILON CHAIN (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RICPR
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MEDLLINE-98019102; PubMed-9358070;

Heckmann S., Schliwa M., Kube-Granderath E.;

Heckmann S., Schliwa M., Kube-Granderath E.;

"Primary structure of Neurospora crassa gamma-tubulin.";

"Primary structure of Neurospora crassa gamma-tubulin.";

Gene 199:303-309(1997).

1- FUNCTION: TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC.)

SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT

IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.

1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUBULIN GAMMA CHAIN (GAMMA TUBULIN).

Neurospora crassa.

Eukaryota; Pezizomycotina; Sordariomycetes;

Eukaryota; Pengi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsiaceae;
NCBI_TaxID=782;
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66.78;
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                                          BACTERIA.
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                                                                                                                                                                                                                                                                                                                                                      NATURE 396:133-140(1998).

-IT FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOANIDE ACETYLTRANSFERASE (E2) & LIPOANIDE DEHYDROGENASE (E3) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99039499; PubMed-9823893;
Andersson J.O.,
Andersson J.C.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
PYRUVATE DEHIDROGENASE E1 COMPONENT, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00929; Exonuclease; 1.
SMART; SM00479; EXOIII; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Exonuclease; Complete proteome.
SEQUENCE 229 AA; 26078 MW; CA7ADE72E6E38D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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STRAIN-MADRID E;
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NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia prowazekii.
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nes 5; Conserv
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N PYROPHOSPHATE + DNA(N).
N PYROPHOSPHATE + DNA(N).
SUBUNIT: COMPAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA SUBUNIT HAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLLII COMPLEX. POLLII ASSOCIATES WITH THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI, AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
                                                                                                                                                                                                     CATALYTIC ACTIVITY: PYRUVATE + LIPOAMIDE = S-ACETYL-DIHYDRO-
LIPOAMIDE + CO(2).
COFACTOR: THIAMINE PYROPHOSPHATE (BY SIMILARITY).
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REIIMD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 39, 1) (Rel. 39, 1) (Rel. 39, 1)
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83.3%;
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InterPro; IPRO00158; FtsZ.

InterPro; IPRO00158; FtsZ.

InterPro; IPRO0006; Tubulin_FtsZ.

R Pfam; pF00091; tubulin; 1.

R PROSTTE; PS01134; FTSZ.1; 1.

NR PROSTTE; PS01135; FTSZ.2; 1.

NR PROSTTE; PS01135; FTSZ.2; 1.

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE-20145173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86 (2000).

1- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
1- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION WILL OCCUR,
THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

1- SUBBURIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).

1- SUBBURIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL DIVISION
FTSZ OR BU212
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20-AUG-2001
20-AUG-2001
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InterPro; IPROID17; EL_dh.
Pfam; PF00676; EL_dehydrog; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on 10 the European Bioinformatics Institute.
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P57308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE FTSZ FAMILY.
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(Rel. 40,
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PROSITE; PS00535;
Oxidoreductase; NA
SEQUENCE 404 AA;
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
135, Last annotation update)
14 promerical 155.4 KDA PROTEIN IN IEO-IEI INTERGENIC REGION.
15 Autographa californica nuclear polyhedrosis virus (AcmnPV).
16 Viruses, debna viruses, no RNA stage; Baculoviridae;
17 Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 3)
30-MAY-2000 (Rel. 3)
NADH DEHYDROGENASE
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STRAIN=C6;
MEDLINE-94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J.,
Ayres complete DNA sequence of Autog
polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ245399; CAB51632.1; -. InterPro; IPR001135; Complex1_49Kd.
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"Rhizobium meliloti carries two sets of nuo genes.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD++) + UBIQUINONE - NADH+) + 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-41;
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Bacteria; Proteobacteria; alpha subdivision;
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                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=46015;
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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35; COMPLEX1_49K; FALSE_NEG
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el. 39, Last sequence update)
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el. 39, Last annotation update)
NASE I CHAIN D 2 (EC 1.6.5.3) (NADH-UBIQUINONE
CHAIN D 2).
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Pred. No. 52;
1; Mismatches
                                                                                         o J., Lopez-Ferber M., Possee R.D.;
Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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RESULT 10 PSAF_HORVU

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Best Local
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                                                                                                                                                                                                              Pfam; PF0
Complete
SEQUENCE
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032163;
30-MAY-2000
30-MAY-2000
20-AUG-2001
                                                                                                                                                                                                                                                          EMBL; 299120; CAB15257.1; -. Subtilist; BG14008; nifU. InterPro; IPR002871; NifU_N. Pfam; PF01592; NifU_N; 1.
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
I- FUNCTION: MAY BE INVOLVED IN THE FORMATION OR REPAIR OF
CLUSTERS PRESENT IN IRON-SULFUR PROTEINS (POTENTIAL).
I- SIMILARITY: BELONGS TO THE NIFU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.

Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

NCBI_TaxID=1423;
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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477 AA; 55417 MW;
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                                                                                                                     Score 25;
Pred. No.
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Pred. No.
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RESULT 11
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Best Local Similarity 83.3
Matches 5; Conservative
THIL_PYRHO 059497;
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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MEDLINE-90033290; PubMed-2680596;
Anandan S., Vainstein A., Thornber J.P.;
Correlation of some published amino acid sequences i polypeptides to a 17 kba LHCI pigment-protein and to IV of the core complex.*;
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01-JUN-1994
15-DEC-1998
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                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                 InterPro; IPR003666; PSI_PsaF. Pfam; PF02507; PSI_PsaF; 1.
                                                                                                                                                                                                                                                                                                                                          EMBL; U08135; AAA68147.1; -. PIR; S06149; S06149. Mendel; 8665; HORVU; PSAF;1.
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Scott M.P., Nielsen V.S., Kn
Submitted (MAR-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
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P13192;
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5 Lett. 256:150-154(1989).

FUNCTION: PROBABLY PARRICIPATES IN EFFICIENCY OF ELECTRON TRANFUNCTION: PROBABLY PARRICIPATES IN EFFICIENCY OF ELECTRON TRANFUNCTION: P700 (OR CYTOCHROME: C553 IN ALGAE AND CYANDBACTERIA). THIS PLASTOCYANIN-DOCKING PROTEIN CONTRIBUTES TO THE SPECIFIC ASSOCIATION OF PLASTOCYANIN TO PS I.

TO THE SPECIFIC ASSOCIATION OF PLASTOCYANIN TO PS I.

SUBCELLULAR LOCATION: ASSOCIATED WITH LUMENAL SIDE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PSAF FAMILY.
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8 (Rel. 37, Last annotation upli
M I REACTION CENTRE SUBUNIT I
17 KDA PROTEIN) (PSI-F).
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yta; Liliopsida; Poales; Poaceae; Pooideae;
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he EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                           CHLOROPLAST.
PHOTOSYSTEM I REACTION CENTILI.
C -> A (IN REF. 2).
S -> E (IN REF. 2).
S -> A (IN REF. 2).
F -> A (IN REF. 2).
REKQ -> HECD (IN REF. 2).
REKQ -> HECD (IN REF. 2).
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III PRECURSOR (LIGHT-HARVESTING
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Matches 5
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20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y. Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Yamamoto S., Otsuka R., Nakazawa H., Takamiya M., Ohfi Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ohoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi Masuchi Y., Shizuya H., Kikuchi H., Gomplete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                       MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Le Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterium aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE THIAMINE-MONOPHOSPHATE KINASE (EC 2.7.4.16) (THIAMINE-
PHOSPHATE KINASE).
THIL OR PH1833.
                                                                                                                                                                                                                                                                                                            AQUAE
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Pfam; PF00586; AIRS; 1.

Thiamine blosyothesis; Transferase

SEQUENCE 309 AA; 34348 MW; 771
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Archaea; Euryarchaeota;
NCBI_TaxID-53953;
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Nature 392:353-358(1998).
                                                                                                                                                       Bacteria; Aquificales;
NCBI_TaxID=63363;
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Bacteria; Aquific
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                                                                                                                               SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE THIAMINE-MONOPHOSPHATE KINASE FAMILY
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5; Conservative
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(Rel. 40,
(Rel. 40,
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, Last annotation update)
AQ_376.
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Pred.
1; Mis
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red. No. 68;
Mismatches
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68;
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ay M.,
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Ohfuku Y.,
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INTEGRAL

MEMBRANE PROTEIN (POTENTIAL)

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Ra Migajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. XIII.

"The complete sequences of 100 new cDNA clones from brain which code

"I for large proteins in vitro.";

LDNA Res. 6:63-70(1999).

LDNA Res. 6:63-70(1999).

LDNA Res. 6:63-70(1999).

LDNA Res. Market S. THE INTRACELLULAR PIP POOL AND TO A LESSER

EXTENT, THE PI 4,5-P(2) POOL. IT GENERATES PIP FROM PI AND, TO A

LESSER EXTENT, PI 4,5-P(2) PROM PI 4-P THERE ARE INDICATIONS THAT

C. IT PHOSPHORYLATES THE D.-5 RATHER THAN THE D.-4 POSITION. HAS A ROLE

C. IN ENDOSOME-RELATED MEMBRANE TRAFFICKING (BY SIMILARITY).

C. HONDPHOSPHATE = ADP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL 4,5-

BISPHOSPHATE = ADP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL 4,5-

BISPHOSPHATE.
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SEQUENCE
                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
FYVE FINEER-CONTAINING PHOSPHOINOSITIDE KINASE (EC 2.7.1.68) (1-
PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE) (PIP5K) (PTDINS(4)P-5-KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                      EMBL; AB023198; BAA76825.1; -. InterPro; IPR002498; PIP5K.
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Mammalia; Eutheria;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    equires a license agreement (See http://www.isb-slb.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the peptide-elongation factor EF-2 gendownstream from those of ribosomal proteins H-S12 and H-S7, archaebacterial extreme halophile, Halobacterium halobium."; Eur. J. Biochem. 186:213-219(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF2_HALHA STANDARD; PRT; 728 AA P14823; O1-APR-1990 (Rel. 14, Created) O1-APR-1990 (Rel. 14, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat ELONGATION FACTOR 2 (EF-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacterium halobium.
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
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OF THE NAS
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                                                                                                                                                                                    X17148; CAA35029.1; -. S07558; S07558.
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PF000679; GTP_EFTU; 1.

ITE; PS00301; EFACTOR_GTP; 1.

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GTP (BY SIMILARITY).
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H-S7, from
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R InterPro; IPR002863; MutS_C.

R InterPro; IPR002863; MutS_C.

R Pfam; PF01624; MutS_C; 1.

R Pfam; PF01624; MutS_C; 1.

R PF0Dom; PD001263; MutS_C; 1.

R PF0Dom; PD001263; MUTS_C; 1.

R PROSTITE; SM00533; MUTSG: 1.

R SMART; SM00533; MUTSG: 1.

R PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
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013921; 013700;
15-DEC-1998 (Rel. 37, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MUTS PROTEIN HOMOLOG 1.

SPAC23C11.18C OR SPAC13F5.01C.
SCh1zosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetaes;
Sch1zosaccharomycetales; Schizosaccharomycetaceae;
Sch1zosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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249 REIVLD 254
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-i- FUNCTION: INVOLVED IN MITOCHONDRIAL DNA REPAIR (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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STRAIN-972;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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29
1 REIIMD 6
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11.135 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_mammal:*
sp_mhc:*
SUMMARIES
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094288 schizosacch	Q9tuql bos taurus	Q9ku86 vibrio chol	Q27657 giardia lam	O92494 bombyx mori	Q911h9 frog adenov	Q64796 autographa	Q12230 saccharomyc	097916 bos taurus	Q9zcy7 rickettsia	Q9ac56 caulobacter	Q9ru01 deinococcus	026645 methanobact	Q9ax28 oryza sativ	059606 pyrococcus	Q9ch00 lactococcus	Q9ma55 arabidopsis	016391 caenorhabdi	Q57935 methanococc	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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066698	099wy0	02285	Q43351	Q9c6w	Q9aha6	Q9rin2	Q54518	052232	P72510	Q3912	Q9aa25	Q9zsu	Q9x4w8	085965	Q9gr40	Q9k7a1	Q9cvs	Q9hku2	Q9z3d8		077033	Q9v8m4	Q48348	Q9r194	CASKA
aquifex aeo	99wy0 staphylococ	022851 arabidopsis	1 arabidopsis	0 arabidopsis	9aha6 streptococc	streptococc	54518 streptococc	streptococc	72510 streptococc	239120 arabidopsis	09aa25 caulobacter	5 oryza sativ	pseudomonas	sphingomona	19gr40 caenorhabdi	19k7al bacillus ha	29cvs2 mus musculu	thermoplasm	streptococc	streptococc	dictyosteli	drosophila		staphylococ	pos caurus

ALIGNMENTS

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TIGR; MJ0515; IPR001135; Complex1_49Kd InterPro; IPR0011501; NiFeSe_Hases			1058-1073(1996) 1058-1073(1996) : NICKEL (BY SIMILARITY) HYDROGEN METABOLISM; FHL PATHWAY (BY SIMI	Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk HP., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus	CYELDEEK R., ALLKHESS E.F., MELISCOK R.G., THELLER CHI, SCOCK R., SCOTT J.L., Geoghagen N.S.M., Weldman J.F., Fuhrmann J.L., Mguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,	MEDILINE-9633/99; PubMed-8088087; Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb JF., Adams M.D., Reich C.I., Ovorbook B. Kitzmass F. Walmstock K.G. Merrick I.M. Glodek A.	NCBI_TaxID=2190; [1] SEQUENCE FROM N.A. STRAIN-JAI-1 / DSM 2661 / ATCC 43067; STRAIN-JAI-1 / DSM 2661 / ATCC 43067;	MJ0515. Methanococcus jannaschii. Archaea; Euryarchaeota; Methanococcales; Methanococcaceae; Methanococcus.	07-793; 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PUTATIVE FORMATE HYDROGENLYASE SUBUNIT 5 (FHL SUBUNIT 5) (HYDROGENASE- 3 COMPONENT E).	ULT 1 935 Q57935 PRELIMINARY; PRT; 380 AA.

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016391;
01-JAN-1998 (TIEMBLIEL:
01-NOV-1998 (TIEMBLIEL:
01-JUN-2001 (TIEMBLIEL:
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston I
Jones M., Kershaw J., Kirsten J., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownker
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00535; COMPLEX1_49K; UNKNOWN_1.
PROSITE; PS00507; NI_HGENASE_L_1; UNKNOWN_1
Hypothetical protein; Oxidoreductase; NAD;
Nickel; Complete proteome.
SEQUENCE 380 AA; 43638 MW; 3EAD16D67834;
                                                                                    Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER
EMBL; AF016443; AAC24282.1; -.
HSSB: P03372; 1HCP
                                                                                                                                                                                                                                                                         *The sequence of C. elegans
Submitted (AUG-1997) to the
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Rhabditidae; Peloderinae;
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STRAIN-BRISTOL N2;
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                                     Pfam; PF00104; hormone_rec; 1 
Pfam; PF00105; zf-C4; 1.
                                                               InterPro;
InterPro;
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                       PRINTS;
                                                                                                                                                       Waterston R.;
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SM00430;
SM00399;
        PRO0047; STROTT
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IPR001628;
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ZnF_C4;
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zf-C4.
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STRAIN-IL1403;
Bolotin A., Wincker P., M
Weissenbach J., Ehrlich S
"The complete genome sequ
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01-JUN-2001
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01-OCT-2000
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01-JUN-2001
F22F7.13 PROFESET.13.
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Zinc-finger.
SEQUENCE 413 AA; 47387 MW;
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EMBL; AC009606; AAF64540.1; -.

InterPro; IPR000582; ACBP.
InterPro; IPR000582; ACBP.
InterPro; IPR001798; Kelch.
Pfam; PP01344; Kelch.
Pfam; PP01344; Kelch.; 5.

SEQUENCE 668 AA; 73074 MW; F99B35A520C0BECA CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                               Lactococcus lactis (subsp. lactis) (Streptococcus Bacteria; Firmicutes; Bacillus/Clostridium group;
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NCBI_TaxID=1360;
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(TrEMBLrel. 15, Last sequence update)
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AK KAWATABAYASI Y., SAWAGA M., HOTIKAWA H., HOSOYYAMA A., NA9AI Y.,

AK YAMAMOTO S., Sekine M., Baba S.-I., KOSUYI H., HOSOYYAMA A., NA9AI Y.,

AK SAKAI M., OGUTA K., OTSUKA R., NAKAZAWA H., TAKAMIYA M., OHUKU Y.,

AK FUNAHASHI T., TANAKA T., KUGOH Y., YAMAZAKI J., KUSHIGA N., OGUCHI A.,

AKAKI K.-I., YOSHIZAWA T., KUGOH Y., YAMAZAKI J., KUSHIGA N., OGUCHI A.,

AKAWATABASHI T., TANAKA T., KUGOH Y., YAMAZAKI J., KUSHIGA N., OGUCHI A.,

AKAWATABASHI T., KIKUCHI H.;

COMPLETE SEQUENCE AND GENE OFGANIZATION OF THE GENOME OF A hyper-

THE THE SEQUENCE AND GENERAL TO THE SECUENCY OF A HYPOTHELICAL PROCESSION MITOCHL CARRIER; UNKNOWN_1.

BY PROSITE: PSO00315; MYD_INA_BING.

BY PROSITE: PSO00315; MYD_INA_BING.

BY PROSITE: PSO00317; MYB_I: UNKNOWN_1.

BY PROSITE: PSO0037; MYB_I: D643F90EA452317F CRC64;
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Best Local S
Matches 5
01-JUN-2001
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SMART; SM00316; S1; I.
PROSITE; PS01175; RIBONUCLEASE_II;
Complete proteome.
SEQUENCE 817 AA; 92250 MW; 440
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EMBL: AE006228; AAX05040.1; -.
InterPro: IPR001900; Ribonuclease_II.
InterPro: IPR003029; S1.
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1; Mismatches
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Pred. No. 3e+02;
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XX MITCH D. R., Doucette-Stamm L. A., DeLoughery C., Lee H.-M., DuBois J.,
XX Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
XX Aldredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
XX Aldredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
XX Aldredge T., Wang Y., Wierzbowski J., Gibson R.,
XX Aldredge T., Sthmer G., Goyal A., Pietrovski J., Prabhakar S.,
XX Aldredge T., Sihmer G., Goyal A., Pietrovski S., Church G.M.,
XX Aldredge T., Mao J.-T., Rice P., Nolling J., Reeve J.N.,
XX Daniels C.J., Mao J.-T., Rice P., Nolling J., Reeve J.N.,
XX Complete genome sequence of Methanobacterium thermoautotrophicum
YT "Complete genome sequence of Methanobacte
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Bukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;

Ehrhartoideae; Oryzeae; Oryza,

MCBI_TaxID-4530;
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0456A01.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002899; BAB21151.1;
SEQUENCE 249 AA; 27391 MW; AD729DA150013E7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID=145262;
                                                                                                                                Q9RU01
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STRAIN-CV. NIPPONBARE;
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4; Conserv
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5; Conservative
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   (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last seq
(TrEMBLrel. 17, Last ann
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                                                                                                                            PRELIMINARY;
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16,
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yta; Liliopsida; Poales; Poaceae;
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Last sequence update)
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Pred. No. 2.6e
1; Mismatches
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   sequence update)
annotation update)
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2.6e+02;
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Q9AC56;
01-JUN-2001
01-JUN-2001
01-JUN-2001
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-I- PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.
-I- SIMILARITY: TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE FAWILY.
EMBL, AE002003; AAF11158.1; -
HSSP; P11411; 1DPG.
TIGR, DR1596; -
                                                                                                                                                       MEDLINE-21173698; PubMed-11259647;
MEDLINE-21173698; PubMed-11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL: AE005675; AAK21993.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last ann
01-JUN-2001 (TrEMBLrel. 17, Last ann
01A, POLYMERASE III, EPSILON SUBUNIT.
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PfAm; PF00479; G6PD; 1.

PRINTS; PR00079; G6PDHDRGNASE.

PRODOM; PD001129; G6PD; 1.

PROSTIE; PS00069; G6P_DEHYDROGENASE; 1.

COmplete proteome; Glucose metabolism; NADP; Oxidoreductase.

SEQUENCE 590 AA; 65600 MM; DA42AEBB4D277722 CRC64;
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-i- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE + NADP(+) - D-GRADERIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE + NADP(+) - D-GLUCOSE 6-PHOSPHATE - D-GLUCOSE 6-PHOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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proteome.
237 AA;
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O97916;
O1-MAY-1999 (TrEMBLrel. 10, C
O1-MAY-1999 (TrEMBLrel. 17, L
O1-JUN 2001 (TrEMBLrel. 17, L
REVERSE TRANSCRIPTASE-LIKE.
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O9ECY7;
O9ECY7;
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAY-1999 (TrEMBLrel. 13, Last annotation updat
""POTHETICAL 37.5 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                RTLF.
Bos taurus (Bovine).
Bos taurus (Bovine).
Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                               SEQUENCE FROM N.A.

Wierinckx A., Mercier D., Oulmouden A., Petit J.M., Julien Wierinckx A., Mercier D., Oulmouden A., Petit J.M., Julien Complete genomic organization of bovine futb gene reveals 5'-untranslated exons of FUT3 and FUT6 have recently emerge encestral intronic sequences.";

submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE TRANSCRIPTASE).

TRANSCRIPTASE).

TRANSCRIPTASE (CANION OF TRANSCRIPTASE).
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STRAIR-MADRID E;

MEDLINE-9030499; PubMed-9823893;

Andersson S.G.E., Zomorodipour A., Andersson J.O.,

Alsmark U.C.M., Podowski R.M.

Eriksson A.-S., Winkler H.H., Kurland C.G.;

"The genome sequence of Rickettsia provazekii and
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EMBL; AJ235272; CAA15012.1; -.
Hypothetical protein; Complete
SEQUENCE 327 AA; 37453 MW;
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NCBI_TaxID=782;
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Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
EMBL; AJ132772; CAA10770.1; InterPro; IPR000477; RVTse.
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i R.M., Naeslund
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                                                                   Hall J., Ahmed A., Bussey H., Fortin N., Friesen J.D., Vo D.H., Wang Y. Winnett E.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases EMBL; Z71255; CAA95037.1; -. EMBL; Z46483; CAA88302.1; -. EMBL; U3335; AAB68101.1; -. SGD; S0005925; YPL004C.
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Q12230;
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MEDLINE-89057455; PubMed-3143101;

O'Hara P.J., Horowitz H., Eichinger G., Young
O'Harb P.J., Horowitz H., Eichinger G., Young
"The yeast ADR6 gene encodes homopolymeric am:
potential metal-binding domain.";
Nucleic Acids Res. 16:10153-10169(1988).
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Walsh S.V., Barrell B.G.;
Submitted (APR-1996) to t
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01-NOV-1996 (TrEMBLrel. 01, Last seque
01-MAR-2001 (TrEMBLrel. 16, Last annot
HYPOTHETICAL 38.1 KDA PROTEIN YPL004C
YPL004C OR LPA13C.
                                               Hypothetical protein SEQUENCE 341 AA;
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MEDLINE-91092258; PubMed=2265610;

Gerring S.L., Spencer F., Hieter P.;

"The CHL 1 (CTF 1) gene product of Saccharomyces

Important for chromosome transmission and normal

progression in G2/M.";

EMBO J. 9:4347-4358(1990).
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Walsh S.V., F
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Badcock K., C
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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RNA-directed DNA polymerase.
SEQUENCE 335 AA; 38403 MW;
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092494;
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Q911H9;
01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                           Davison A.J., Wright K.M., Harrach B.;
"Phylogenetic position of an amphibian adenovirus.";
"Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF224336; AAF86928.1;
"InterPro; IPR002605; Adeno_Penton_B.
Pfam; PP01866; Adeno_Penton_B; 1.
SEQUENCE 445 AA; 50029 MW; E5061EFB041CB0CD CRC64;
                                                                                                                                                                                                                          Frog adenovirus 1.
Viruses; dsDNA viruses,
NCBI_TaxID=114102;
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Viruses; dsDNA viruses,
Nucleopolyhedrovirus.
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Pred. No. 4.4e+02;
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D7 01-NOV-1998 (TREMBLTel. 08, Last sequence update)
D7 01-NOV-1998 (TREMBLTel. 08, Last annotation update)
D8 ACMNEV ORF142.
OS BOMDYX MORIT NUCLEAR POLYHEDROSIS VIRUS (BMNPV).
OC VIRUSES; dSDNA VIRUSES, NO RNA Stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TAXID-10458;
RN 1(1)
RP SEQUENCE FROM N.A.
RC STRAINE-9729351; PubMed-9185864;
RX MEDLING-9729351; PubMed-9185864;
RX KAMILAS G., Maeda S.;
RX KAMILAS G., Maeda S.;
RX KAMILAS G., Maeda S.;
RY "Sequencing of the putative DNA helicase-encoding gene of the Bombyx mori nuclear polyhedrosis virus and fine-mapping of a region involved RT in host range expansion.";
Cane 190:173-179(1997).
RN [2]
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-T3;
RA Gomi S., Majima K., Maeda S.;
RY "Sequence analysis of the genome of Bombyx mori RT sequence analysis of the genome of Bombyx mori RT sequence analysis of the genome of Bombyx mori RT sequence analysis of the genome of Bombyx mori RT sequence analysis of the genome of Bombyx mori RT Sequence A76 AA; 55375 MM; ACOE60102260906B CRC64;
Ouery Match 89.7%; Score 26; DB 12; Length 476; Best Local Similarity 83.3%; Pred. No. Se+02; Best Local Similarity 83.3%; Pred. No. Se+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0, 11111 Db 320 REIILD 325

Search completed: March 18, 2002, 09:51:59

Job time: 288 sec
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                    Score
                                                                                                                                                                                 Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         March 18, 2002, 09:48:56; Search time 81.32 Seconds (without alignments) 5.465 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEIIMR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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                                                                                                                                                                                    Length DB
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                                              AAY01814
AAB95262
AAW84351
AAB31162
AAW10344
AAG98338
AAR82886
AAW31227
                                                                                                                                                                                                                                SUMMARIES
Peptide used to re Human protein seque Murine ubiquitin-p Amino acid sequenc Malze dwarf mosaic Escherichia coli p Human leucine zipp Human leucine-zipp Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AAY01814
      Cines D,
                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                   Abnormal cell migration; PAI-1 dependent cell adhesion; scuPA clearance pathological cell migration; angiogenesis; organogenesis; ovulation; inflammation; cancer; tumor cell invasion; metastasis; atherosclerosis.
                                                                                                                                                                                                                              29-APR-1999.
                                                                                                                                                                                                                                                            W09920295-A1.
                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY01814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY01814 standard; peptide; 6 AA
                                                                                                                                                                     17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                              Peptide used to regulate scuPA.
                                                                                                                                                                                                15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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ALIGNMENTS

scuPA clearance;

Example 1; Page 31; 63pp; English WPI; 1999-288168/24 (UYPE-) UNIV PENNSYLVANIA. Peptide composition Higazi AA; 97US-0062274. 98WO-US21800

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Query Ma
Best Loc
Matches
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T,
Ishii :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptides AAYO1812-14 exemplify the peptide of the invention, which is used in a peptide composition to affect a biological process characterized by abnormal cell migration through a physiological barrier, to inhibit PAI-1-dependent adhesion of a cell to a tissue, to promote clearance of scuPA from the surface of a mammalian cell, and to impede pathological migration of a cell in a mammal. The composition can be used to affect a biological process characterized by abnormal cell migration through a physiological barrier, where the process is selected from anglogenesis, organogenesis, ovelation, inflammation, cancer, tumor cell invasion and metastasis, and atherosclerosis.
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence complementary to a polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which comprises a by-end sequence and an oligonal polynucleotide which com
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                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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, Sugiyama
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                                                                                                                                                                                                                                                         SEQ ID 17446; 2537pp +
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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A, Nagai K,
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K, Otsuki
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ubiquitin-protein ligase; Ubrl; mouse; N-end rule pathway; stress-related musc
                     The present sequence represents a ubiquitin-protein ligase called Ubr1. The Ubr1 enzymes are involved in protein ubiquitinylation and ultimate degradation through the N-end rule pathway and have been linked to stress-related muscle wasting. Recombinant Ubr1 polypeptides can be used to screen for inhibitors of muscle wasting when this is associated with the N-end rule pathway.
                                                                                                                      Disclosure;
                                                                                                                                            Mouse and human Ubrl cDNA polypeptides
                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                   02-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine ubiquitin-protein ligase Ubrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1999
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Sequence
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                                                                                                                      Columns 15-28;
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83.
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                                                                                                                                                                                                                                                           TECHNOLOGY.
                                                                                                                      18pp; English
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1; Mismatches
                                                                                                                                                               useful for producing
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                                                                                                                                                                                                                                                                                                                                                                                                                       muscle wasting; inhibitor; screen.
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                                                                                                                                                               recombinant
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Query Match Best Local S Matches 5

Similarity 83. 5; Conservative

96.4**%**; 83.3**%**;

Score 27; DB Pred. No. 6.7e 1; Mismatches

.7e+02; 0;

Indels

0

Gaps

0

DB 20;

Length 1757;

Maize dwarf mosaic virus polyprotein

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Query Match
Best Local Similarity
Tatches 5; Conserve
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AAB31162
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                                                                                                                                                                                           The present sequence represents a murine Ubrl enzyme. Ubrl is an E3-type protein of the ubiquitin system. Specifically, it is a ubiquitin protein ligase. The enzyme is specific for destablising residues exposed at the N-terminus of protein substrates. Inhibition of the expression of Ubrl gene in a cell results in inhibition of the N-end rule pathway. The method is used for treatment of mammailan cells infected with an intracellular pathogen, e.g. Lysteria monocytogenes or Yersinia enterocolitica. Inhibition of N-end rule pathway is also useful for treating various diseases associated with wasting of muscle tissue and
                                                                                                                                                                                                                                                                                                      Inhibiting the N-end rule pathway in mammalian cells for treating infections and various diseases associated with muscle tissue wasting, by inhibiting the expression of Ubrl gene
 15-APR-1997
                 AAW10344;
                                   AAW10344 standard;
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                      Example; Column 15-28; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Kwon YT, Varshavsky A;
                                                                                                                                                                                                                                                                                                                                                                                         (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6159732-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubr1: E3-type protein; ubiquitin system: ubiquitin-protein ligase;
N-end rule pathway: intracellular pathogen; Lysteria monocytogenes;
Yersinia enterocolitica; muscle wasting; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of Mouse Ubrl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB31162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB31162 standard; Protein; 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEIIMR 6
||:|||
765 eevimr 770
                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                765 eevimr 770
                                                                                                   1 EEIIMR 6
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                                                                                                                                                                                                                                                                                                                                             2001-090278/10.
DB; AAC86933.
                                                                                                                                                                  1757 AA;
                                                                                                                     Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            97US-0982956.
                                                                                                                                                                                                                                                                                                                                                                                                                             9905-0228317
                                   Protein; 2763 AA
                                                                                                                    Score 27; DB Pred. No. 6.7e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ⋧
                                                                                                                             DB 22;
6.7e+02;
                                                                                                                     0,
                                                                                                                                     Length 1757;
                                                                                                                    Indels
                                                                                                                    0
                                                                                                                    Gaps
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/note=
Misc-difference 712
                                                                                                                                                                                                                                                                                                                                                                              /note= "unidentified Misc-difference 704
30-JUN-1995;
                                                                                                                       Misc-difference
                                                                                                                                                Misc-difference
                                                                                                                                                                    /note=
Misc-difference 1362
                                                                                                                                                                                                    Misc-difference 1346
                                                                                                                                                                                                                  /note=
Misc-difference 852
                                                                                                                                                                                                                                          /note-
Misc-difference 847
                                                                                                                                                                                                                                                                   /note-
Misc-difference 843
                                                                                                                                                                                                                                                                                               /note=
Misc-difference 834
                                                                                                                                                                                                                                                                                                                         /note-
Misc-difference 829
                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDMV-B; viral resistance; disease resistance; transgenic plant; monocot; P3 proteinase; NIa proteinase; NIb replicase; RNA-dependent RNA polymerase; coat protein; Zea mays; sorghum; sugarcane; Saccharum officinale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                         20-JUN-1996;
                                                     23-JAN-1997.
                                                                               W09702352-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize dwarf mosaic virus strain B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
 95US-0496944
                            96WO-EP02673.
                                                                                                                                                  /note=
2077
                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Coat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               2436..2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263..336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label* HC-Pro
/note* "portion of the helper component-P2
proteinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Nia_proteinase
/note= "claimed polypeptide (Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                    'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= NIb_replicase
note= "claimed polypeptide (Claim 20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Cylindrical_inclusion_protein
/note= "claimed polypeptide (Claim 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= P3_proteinase
note= "claimed polypeptide (Claim 20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "conserved helicase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1010
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                                                                                                                                                                                                                                                                                               "unidentified
                                                                                                                                                                                                                                                                                                                         "unidentified
                                                                                                                                                                                                                                                                                                                                                  "unidentified
                                                                                                                                                                                                                                                                                                                                                                           "unidentified amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "6 kDa protein"
                                                                                                                                   "unidentified
                                                                                                                                                              "unidentified
                                                                                                                                                                                                                "unidentified
                                                                                                                                                                                                                                        "unidentified
                                                                                                                                                                                                                                                                     "unidentified
                                                                                                         "unidentified amino
                                                                                                                                                                                       "unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "MDMV-B HC-Pro domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved motif characteristic of RNA-dependent replicases
                                                                                                                                                                                                                                                                                              amino acid"
                                                                                                                                    amino
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(CIBA) CIBA GEIGY AG

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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of the polyprotein encoded by the polycistronic mRNA (AA747073) of malze dwarf mosaic virus strain B (MDWV-B) is given in AAW10344. New chimaeric genes comprise a monocotyledonous plant promoter linked to a modified nucleic acid sequence derived from the MDMV-B genome. The modification is such that mRNA is translated to a truncated protein (pref. smaller than 200 amino acids), no translation of mRNA occurs or the transcribed mRNA lacks the translation initiation codon or includes a premature stop codon. Expression of the chimaeric gene inhibits infection of plants (pref. sorghum, sugarcane, esp. malze) by MDMV. The transgenic plants display an inheritable resistance trait.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 31-44; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimaeric gene for imparting viral resistance to plants - contains sequence modified to express non-translatable mRNA, or non-coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dietz JM,
                                                                                                                                                                                                                                                    05-JUL-2001.
                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                  Escherichia coli; identification; antimicrobial; antibacterial; anti
                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli protein sequence SEQ ID NO:386
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG98338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG98338 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2064 eeivmr 2069
                         Claim 19; Page 507-508; 596pp; English.
                                                                                           WPI; 2001-457376/49.
N-PSDB; AAH81394.
                                                                                                                                                                                                                       19-DEC-2000; 2000WO-US34419
                                                                                                                                                                                                                                                                                WO200148209-A2
                                                                                                                                                                                                                                                                                                                                    bacterial growth inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2001 (first entry)
                                                   Novel nucleic acids encoding proteins required for Escherichia proliferation, useful for screening for antimicrobial agents -
                                                                                                                                       Forsyth RA,
                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EEIIMR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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DB; AAT47073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2763 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                       Ohlsen KL,
                                                                                                                                                                                            99US-0173005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.4%;
                                                                                                                                       Zyskind JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
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Pred. No. 1.1e+03;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                               ion; proliferation; microorganism;
antibiotic; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                   coli
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The present invention describes a purified or isolated nucleic

acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR82886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
          This novel protein may be used to treat tumors of the CNS in mammal by inhibiting the overexpression of the leucine zipper protein-kinase in vivo, or by interfering with a vital signal in a chain of signals leading to tumorigenicity.
                                                                                                                                   DNA encoding novel leucine zipper polypeptide(s) prepared using the
                                                                                                                                                                                     WPI; 1995~320565/41.
N-PSDB; AATO1031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leucine zipper protein-kinase; enzyme; zpk; CNS; diagnosis; central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                        Claim 4; Page 23-27; 40pp; English.
                                                                                                                     polypeptide(s) prepared using the hyper-proliferation of CNS cells
                                                                                                                                                                                                                                     Pleasure DE,
                                                                                                                                                                                                                                                                 (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
                                                                                                                                                                                                                                                                                                 01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                              W09523849-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leucine zipper protein-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR82886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR82886 standard; Protein; 859 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 qeiimr 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEIIMR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                   Reddy
                                                                                                                                                                                                                                                                                                 94US-0205018.
                                                                                                                                                                                                                                                                                                                                 95WO-US02792
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                          protein kinase - also probe(s)
DNA, useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 246;
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Query Match
Best Local S
Matches 4
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Misc-difference 292
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Misc-difference 278..280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Mentioned Misc-difference 254..256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Mentioned Misc-difference 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Mentioned in Misc-difference 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227
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Misc-difference 236..237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leucine zipper protein kinase; zpk; human; metastasis; tumour; serine/threonine protein kinase; non-receptor type kinase; cell hyperproliferation.
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leucine-zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW31227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31227 standard; Protein; 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                            /note= "Mentioned in Misc-difference 450
                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-1998 (first entry)
             US5676945-A
                                                                                                                    Misc-difference
                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                           Misc-difference 443
                                                                                                                                                                                                                                                                                Region
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4; Conserv
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                                                                                                                    464
                                                                                                                                                                                                                                                               442..468
/label- I
                                                                                                                                                                                                                                                                                                                                                                       /note- "Mentioned
297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= protein_kinase_domain
/note= "As stated in specification"
234.235
                                                                                     /note= "Mentioned in 537..544
                                                                                                                                                        /note= "Mentioned in 457
                                                                                                                                                                                                                                                                                                                                    /note= "Mentioned in specification" 415..418
                                                                                                                                                                                                                                                                                              /note- "Putative endoplasmic reticulum targeting sequence as given in the specification"
                                                                                                                                                                                                                                           /label= Leucine_zipper_motif
/note= "As stated in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= zpk
/note= "leucine zipper protein kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cocation/Qualifiers
                                                                                                                                    note- "Mentioned in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase.
                                               - ATP_binding_site
"As stated in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mentioned in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mentioned in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mentioned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB
Pred. No. 9.4e
2; Mismatches
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9.4e+02;
ches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC isolated from brain tissue. The specification states that the protein contains an ATP-binding site at position 537-544 (consensus CC sequence Gly-Xaa-Gly-Xaa-Xaa-Gly), a protein kinase domain at position CC 231-243 and a putative endoplasmic reticulum (ER) targeting sequence at CC position 413-418 (consensus sequence REEL). This protein is most similar CC to members of serine/threenine protein kinases and is believed to be a "mon-receptor type kinase" based on its lack of a transmembrane domain. CC probes to this protein could be used for diagnostic or research purposes CC to detect or quantitate the expression of leucine-zipper protein kinase. CC propession of leucine zipper protein kinase can result in the protein colls and metastasis. The application of exogenous cor protein roucleic acid interactions involved in hyperproliferation. This can be used to treat animals suffering from tumours of the central CC nervous system by inhibiting the overexpression of leucine-zipper protein constitutions involved in hyperproliferation. This can be used to treat animals suffering the overexpression of leucine-zipper protein constitutions involved in hyperproliferation. This can be used to treat animals suffering the overexpression of leucine-zipper protein constitutions involved in hyperproliferation of constitu
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01-MAR-1994;
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25-FEB-1999;
                                 25-FEB-2000;
                                                                   06-SEP-2000
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                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                          termination sequence.
                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                    18-OCT-2000
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N-PSDB; AAT89349.
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94US-0205018.
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01-APR-1999

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                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 59313.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG47089;
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Similarity 83.3%;
5; Conservative
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990S-0161106
990S-0161104
990S-01611404
990S-0121825
990S-0123180
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990S-0126786
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990S-0126785
990S-0126783
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Pred. No. 1.2e+03;
1; Mismatches 0
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promoter;
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RESULT 11
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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| ee11mk 26
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5; Conservative
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Pred. No. 1.3e+03;
1; Mismatches 0; Indels
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AAW95359
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26-OCT 1999
The invention relates to a human interleukin (IL)-1 alpha propiece polypeptide. The polypeptide has activity in the selective induction of apoptosis in cancer cells. The IL-1 alpha propiece polypeptide or its variants which retain the apoptosis-inducing activity are used in compositions and methods to selectively induce apoptosis in cancer cells, especially manignant cancer cells. The polypeptides form the basis for effective, apoptotic-based chemotherapy where apoptosis-inducing agents
                                                                                                                                                                                                    27-MAY-1998;
30-MAY-1997;
                                                                                                                                                                                                                                                                                                      Interleukin;
cancer; cell
                                                                             Disclosure;
                                                                                            New polypeptides comprising an apoptosis-inducing domain and a
heterologous nuclear localisation sequence - useful for, e.g.
forming compositions and methods for selectively inducing apoptosis
in cancer cells
                                                                                                                                             WPI; 1999-059804/05
                                                                                                                                                                Lovett DH,
                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                              28-MAY-1998;
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1-OCT-1999;
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5; Conservative
                                                                             Page 65-66; 88pp; English
                                                                                                                                                                Pollock AS,
                                                                                                                                                                                                                                                                                                        IL-1 alpha propiece; apoptosis; variant; malignant; death.
                                                                                                                                                                                                                                                                                                                                                      (first entry)
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990S-0161406.
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97US-0048137
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Pred. No. 1.4e+03;
1; Mismatches 0;
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Tn5401 is present in B.t. var. morrisoni strain E02158 (NRRL-B-18213). E02158 was transformed with donor plasmid pE0911 and recombinant plasmids were analyzed. 2 Contained a 5 kb insert (given in AAQ85492) including 2 ORFs encoding a resolvase (AAR659825) and a transposase (AAR75354). Tn5401 is used in site-specific recombination to construct improved B.t. strains for biological
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 49-58; 106pp;
                                                                                                                                                                                                                                                                                                                                                              New transposon {\tt Tn5401} from Bacillus thuringiensis and fragments of it - and related plasmids and transformed B. thuringiensis useful as insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-066902/09.
N-PSDB; AAQ85492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1993;
24-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transposon; Tn5401; resolvase; insecticide; biological control agent; site-specific reco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               selectively trigger cell death in cancerous cells, but do not harm surrounding normal tissue. The present sequence represents a canine IL-1 alpha propiece polypeptides of non-human origin can be derived from such precursor polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-1994;
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                                     Similarity 66.
4; Conservative
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4; Conserv
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94US-0266408
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66.7%;
                                                      85.7%;
                                  Score 24; DB
Pred. No. 5.6e
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Pred. No. 4.9e+02;
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                              ).6e+02;
0;
                                                                            DB 16;
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recombination;
                                                                          Length 306;
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AAY81702
ID AAY8
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Tatches 4; Conserve
                                 RESULT 15
                                                                                                                                                                                                                                                                  thuringiensis transposon Tn5401. The transposable element Tn5401 ce encodes 'recombinase/resolvase' and transposase gene products, which cenables a desired gene product (the toxin) to be transferred between bacterial strains. This is used in a method for site-specific recombination system for construction of recombinant B. thuringiensis strains. These strains contain insecticidal toxin protein genes and are free of DNA not native to B. thuringiensis. Insecticidal compositions containing these B. thuringiensis strains are used in insect control methods. The B. thuringiensis strains are used in the compositions produce proteinaceous crystalline inclusions during sporulation, which are highly toxic to specific insects, e.g. Spodoptera and lepidopteran species. The plasmids used enable genes not native to B. thuringiensis to be transferred to strains. Previous genetic transfer of plasmids relied on conjugation, which does not always enable the foreign gene product to be expressed in B. thuringiensis, and plasmids that do transfer, sometimes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-SEP-1996;
08-JUL-1993;
24-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. thuringiensis transposon Tn5401 resolvase protein.
 AAY81702 standard; Protein; 314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This represents the resolvase protein encoded by tnpI of the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1A-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insecticidal recombinant Bacillus thuringiensis strains - contain transposable elements for expression of recombinant insecticidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-397942/34.
N-PSDB; AAV34699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW60180 standard; Protein; 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ECOG-) ECOGEN INC
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                                                                                                          1 EEIIMR 6
                                                                                edvimr 177
                                                                                                                                                                                                                                                       undesirable genes
                                                                                                                                                                                                                           306 AA;
                                                                                                                                            Conservative
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93US-0089986.
94US-0266408.
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                                                                                                                                                           85.78;
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                                                                                                                                            Score 24; DB
Pred. No. 5.6e
2; Mismatches
                                                                                                                                            DB 19; I
5.6e+02;
thes 0;
                                                                                                                                                                           Length 306;
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Search completed: March Job time: 366 sec

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||:|:| 145 eevilr 150

1 EEIIMR 6

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This sequence represents a Streptococcus pneumoniae protein of the cinvention. The proteins (or their homologues, derivatives and/or cragments) are useful as immunogens or antigens. Immunogenic or antigenic cc compositions comprising the proteins are useful as vaccines and also in compositions comprising the proteins are useful as vaccines and also in contacting a sample to be tested compositions of S. pneumoniae infection, by contacting a sample to be tested composition or expression of the protein or polypeptide are useful in the function or expression of the protein or polypeptide are useful in compositions in the treatment or prophylaxis of S. pneumoniae infection, as the sequences can be used to treat S. pneumoniae infection, as the sequences can be used to treat S. pneumoniae infection, compositions to the elderly, and in patients with predisposing conditions could be separated by the elderly and kidney disease, diabetes, alcoholism, composition in the content of the protein 
Query Match
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Matches 4
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                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 37; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcal proteins and polynucleotides useful for diagnosis, treatment and prophylaxis of bacterial infections
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19-MAR-1999;
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                                                                                                                                                                           neningitis
                         Local Similarity
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     Conservative
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99US-0125329.
                            85.7%;
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  Score 24; DB 21;
Pred: No. 5.8e+02;
2; Mismatches 0;
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                                                  Length 314;
     Indels
     0;
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Result
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Match
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28
1 EEIIMR 6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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US-08-496-944-2

US-08-395-580-2

US-08-395-580-2

US-08-395-965-2

US-08-08-9-965-2

US-08-08-17-313-2

US-08-18-614-25

US-08-18-614-25

US-09-138-614-25

US-09-138-614-25

US-09-138-614-25

US-09-138-614-25

US-09-138-614-25

US-09-138-614-25

US-09-138-71-62D-46

US-08-71-62D-46

US-08-71-62D-46

US-08-159-417-2

US-09-159-417-2

US-09-12-871-6

US-08-477-112-6

US-08-313-4812-6

US-08-313-4812-6
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Conservative

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Mismatches

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Query Match  96.4%; Score 27; DB 3; Length 2763  Best Local Similarity 83.3%; Pred. No. 3.3e+02;  Matches 5. Conservative 1: Mismatches 0: Indels	ATION: Law, Marcus D Dietz, Jon M ENTION: Confer Resi ENTION: Confer Resi ENTION: Monocotyled QUENCES: M CE ADDRESS: CIBA-Geigy Corpora SKyline Drive thorne	8-840-204-2 9-348-817A-4 9-026-408-3 8-889-841B-10 8-889-841B-12 8-889-841B-2 8-889-841B-2 8-889-841B-5 8-889-841B-5 8-487-2240A-16 8-467-822-30 8-432-697-30 8-432-697-30 8-432-697-30 8-436-626-6 8-466-626-6 8-466-626-6 8-466-6519-12 9-257-490-13
o. Gans.	ic Virus and Other	Sequence 2, Appli Sequence 3, Appli Sequence 8, Appli Sequence 10, Appl Sequence 10, Appl Sequence 12, Appl Sequence 16, Appl Sequence 2, Appli Sequence 5, Appli Sequence 30, Appl Sequence 30, Appl Sequence 6, Appli Sequence 12, Appli Sequence 12, Appli

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; MOLECULE TYPE: protein US-08-205-018-2
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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 668 amin
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409 EELVMR 414
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn_Release #1.0, Version #1.25
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CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Usharani R. Reddy, David Pleasure and the Children's PPLICANT: Hospital of Philadelphia Protein Kinase, Nucleic Acid TILE OF INVENTION: Sequences Encoding the Same and Methods Relations of the Same an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 4; Conserv
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               MBER OF SEQUENCES:
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                                                                                                                                                          COUNTRY:
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ESPONDENCE ADDRESS:
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5, 5676945
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                                                                  inch disk, 720 Kb
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uences Encoding the Same and Methods Related Thereto
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Pred. No. 2
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; MOLECULE TYPE: protein US-08-395-580-2
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PCT-US95-02792-2
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NFORMATION FOR SEQ ID NO: 2:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/20
FILING DATE: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                        APPLICATION NUMBER: 08/2
FILING DATE: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Usharani R. Reddy, David Pleasure and the Children's APPLICANT: Hospital of Philadelphia
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acid
                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.
                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                    NAME: Rebecca L. Ralph (formerly Gaumond)
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH-0488
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                   ELEPHONE:
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ESTRATION NUMBER: 3
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amino acid
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One Liberty Place - 46th Floor
   859 amino acids
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SYSTEM: PC-DOS/MS-DOS
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Sequences Encoding the Same and Methods Related Thereto
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protein

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; MOLECULE TYPE: PCT-US95-02792-2
RESULT 6
US-08-089-986-2
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Best Local
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NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 65.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                     MOLECULE TYPE: No. 6191269e
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Selective Induction of Apoptosis in TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-TVTITLE OF INVENTION: Interleukin-l-Alpha Pro-Piece Polypeptide NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pollock, Allan
APPLICANT: Lovett, David H.
APPLICANT: Turck, Johanna
                                                             101 EEVIMK 106
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                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
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CITY: Palo Alto
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OPERATING SYSTEM: DOS
                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                           1 EEIIMR 6
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amino acid
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29-MAY-1998
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                                                                                                                       Score 24; DB 4;
Pred. No. 1.7e+02;
2; Mismatches (
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                                                                                                                                                      Length 265;
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Query Match
Best Local Similarity
Watches 4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1591
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: (
                                                                                                                                                                                                                                                                                                                             APPLICANT: Baum, James A.
TITLE OF INVENTION: Bedillus thuringiensis Transposon Tn5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 EDVIMR 177
                                                                                                                                                                         STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                           ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S ADDRESSEE: Nadel
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Philadelphia
Pennsylvania
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66.7%;
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Pred. No. 2e+02;
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; MOLECULE TYPE: protein US-08-478-585-2
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Best Local Similarity
Query Match

Best Local Similarity bo.,

Chas 4; Conservative
                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/266,408

FILING DATE: 24-JUL-1994

APPLICATION NUMBER: US 08/089,986

APPLICATION NUMBER: 08-JUL-1993

INFORMATION FOR SED ID NO: 2:

SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/
FILLING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linn
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                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 EDVIMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILE OF INVENTION: Bacillus thuringlensis Transposon Tn5401
TILE OF INVENTION: and Its Use in a Site-Specific Recombination System For INVENTION: Recombinant Bacillus thuringlensis Strain Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEIIMR 6
                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 72
LECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 07-JU
                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. Nadel
T: 1601 Market Street, 36th Floor
Philadelphia
Phensylvania
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                                                                                                                                               linear
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07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         James A.
                                      85.7%;
66.7%;
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66.7%;
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                         Score 24; DB
Pred. No. 2e+0
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 1; Length 306;
pred. No. 2e+02;
2; Mismatches 0; Indels
                                        DB 1;
2e+02;
                                                        Length 306;
                         0; Indels
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                                                                                                                                                                                                                                                                                                                                   PCT-US94-07886-2
                                                                                                                                                                            Sequence 2, Application PC/TUS9407886
GENERAL INFORMATION:
APPLICANT: Baum, James A.
TITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,986
FILING DATE: 08-JUL-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                           172 EDVIMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66. hes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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                                                                                        STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                 CITY: Philadelphia
                                                                                                                                                STREET:
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                                                                            19103
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amino acid
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1601 Market Street, 36th Floor
                                                                                                                                                E: Panitch Schwarze Jacobs & Nadel c/o A.S. Nadel 1601 Market Street, 36th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis Transposon Tn5401 and Its Use in a Site-Specific Recombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant Bacillus thuringiensis Strain Development
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Pred. No. 2e+02;
2; Mismatches
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FILING DALE.

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/391,000

FILING DATE: 21-FEB-195

ATTORNEY/AGENT INFORMATION:

NAME: DAGIO, SUSSIN M.

REGISTRATION NUMBER: 40,373

REFERENCE/DOCKET NUMBER: 028750-13

TELECOMMUNICATION INFORMATION:

TFILEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
""" (Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-687-916-25; A
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INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                 TELEFAX: (703) 836-2021
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA; APPLICATION NUMBER: US/08/687,916 FILING DATE: 29-UUL-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,986
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 EDVIMR 177
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ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOA STREET: P.O. Box 1404 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY: United States 22313-1404
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                linear
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                          single
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RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
SUBUNIT N. METHYLTRANSFERASE AND METHOD OF INACTIVATING
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT N-METHYLTRANSFERASE ACTIVITY
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                                                                                                       25:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 5; Length 306
Pred. No. 2e+02;
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RESULT 13
US-09-315-793-12
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GENERAL INFORMATION: APPLICANT: Roberts, Christopher J.
                               Sequence 12, Application US/09315793 Patent No. 6221597
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
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Matches
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Best Local
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                               1 EEIIMR 6
||:|:|
196 EEVILR 201
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,916
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196 EEVILR 201
                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Dadio, Susan M. REGISTRATION NUMBER: 40,373 REFERENCE/DOCKET NUMBER: 02 TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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5. 6245541
                                                                                                                                                                                                                                                                                                                                                490 amino acids amino acid
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4; Conservative
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OR SEQ ID NO: 25:
                                                                                                                                                                                                  Conservative
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ISOLATED SPINACH
ISOLATED SPINACH
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/138,614
                                                                                                                                                                                                Score 24; DB 4;
Pred. No. 3.1e+02;
2; Mismatches 0
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US-08-781-020-6
Sequence 6, Application US/08781020
Patent NO. 5792749
GENERAL INFORMATION:
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; SEQ ID NO 12
; LENGTH: 1698
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-315-793-12
                  Ş
                                                                                                                                                               ; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-781-020-6
                                                         Ouery Match

92.1%; Score 23; DB 1;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 5; Conservative 0; Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
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CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION TITLE OF INVENTION: DRUGS
                                                                                                                                                                                                                                                                NFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/781,020
FILING DATE: 09-AN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 EEIIVR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
1 EEIIM 5
                                                                                                                                                                                                                                                                                                                                                 NAME: Whitham, Michael E. REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: VCU-16
LLECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: WHITHAM, CURTIS, WHITHAM & McGINN
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW TILE OF INVENTION: DENSITY LIPOPROTEIN CHOLESTEROL
                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEIIMR 6
                                                                                                                                                                                                                                                                                                                                   703-391-9035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 4; Length 1698; Pred. No. 1e+03;
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                                                              0:
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                                                              Indels
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-038-935-6
Search completed: March 18, 2002, 09:49:42
Job time: 226 sec
                                                                                                                                                         Query Match
Best Local Similarity
Thes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/038,935
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 08/781,020
EARLIER FILING DATE: 1997-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-038-935-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Janciauskiene, Sabina
ITLE OF INVENTION: METHOD AND COMPOSITION FOR LOWERING LOW DENSITY
ITLE OF INVENTION: LIPOPROTEIN CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: Wright, H. Ton
PPLICANT: Janciauskiene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LE REFERENCE: 294022ba
                                                                                                                                    1 EEIIM 5
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                                                                                                  EEIIM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Application US/09038935 6150332
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. Tonie
                                                                                                                                                                        82.1%; Score 23; DB 4; Length 33; 100.0%; Pred. No. 39; Live 0; Mismatches 0; Indels
                                                                                                                                                                             0;
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200 이 12 1일 보고 12 이 경험이 되는 것이 되었다. 12 1일	
경기 선생님 전체 기계 시간	
. 이 사용 (1985년 1월 1일 - 1985년 - 1987년 - 1987년 - 1985년 - 1985년 1987년 - 1985년	
다는 사람들이 되었다. 그는 사람들은 사람들이 되었다. 그런 사람들이 되었다. 일반 사람들이 되었다. 그는 사람들이 가장 보는 것이 되었다. 그는 사람들이 되었다.	
수 있는 경험에 되는 것이 되었다. 그런 그는 것이 되었다. 그런	
전체의 발생한 사람들은 가장 되는 사람이 많아 전해서 보면 학생들은 사회 전쟁을 받는 것으로 보는 수 있다. 대한 사람들은 사용하는 사용이 되었다. 그는 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은	
보다는 사람이 가면 가고싶다가 됐다면 나가 가지 않는데 그 그들은 사람이 나는 하는데 그리고 가고싶다.	

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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length: 2000000000
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28
      219241 segs, 76174552 residues
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pir2: *
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   G82350
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JC5318
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JC575113
JC575121
S60525
E83022
C72617
G64602
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                                                                                                         hypothetical prote
hypothetical prote
envelope polyprote
probable glycosyl
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hglC protein - Ana
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DNA polymerase hom
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probable dipeptide
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A;Gene: Ubr
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A;Molecule type: mRNA
A;Residues: 1-1757 <KWO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Accession: 714318
R:Kwon, Y.T.; Reiss, Y.; Eried, V.A.; Hershko, A.; Yoon, J.K.; Gonda, D.K.; Sangan, Proc. Natl. Acad. Sci. U.S.A. 95, 7898-7903, 1998
A;Title: The mouse and human genes encoding the recognition component of the N-end A;Reference number: 217977; MUID:98318583
A;Recession: 714318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ubiquitin-protein ligase E3-alpha - mouse
N;Alternate names: N-recognin E3-alpha
C;Species: Mus musculius (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF061555; NID:g3170886; PID:g3170887; PIDN:AAC40165.1
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## ALIGNMENTS

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conserved hypothetical protein MTH1148 - Methanobacterium thermoautotrophicum (strai c; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Decies: Methanobacterium thermoautotrophicum C; Decies: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C; Accession: H69019 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C; Accession: H69019 #sequence revision 05-Dec-1997 #text_change 22-Oct-1999 C; Accession: H69019 #sequence of Methanobacterium thermoautotrophicum Delta H: f A; Reference number: A69000; MUID:98037514 A; Accession: H69019 #UID:98037514 A; Accession: H69019 #tree-num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
"a+ches 5; Conserva
A;Cross-references: GB:AE000884; GB:AE000666; NID:g2622242; PIDN:AAB85637.1; PID:g26
A;Experimental source: strain Delta H
C;Genetics:
                                                                             A; Molecule type: DNA
A; Residues: 1-157 < MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:|||
| 765 EEVIMR 770
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83.3%;
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Pred. No. 2.8e+02;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A,Residues: 1-498 <SIM>
A;Residues: 1-498 <SIM>
A;Cross-references: GB:AE004011; GB:AE003849; NID:g9107007; PIDN:AAF84720.1; GSPDB:GN001
A;Cross-references: GB:AE004011; GB:AE003849; NID:g9107007; PIDN:AAF84720.1; GSPDB:GN001
A;Cross-references: GB:AE004011; GB:AE003849; NID:g9107007; PIDN:AAF84720.1; GSPDB:GN001
A;Experimental source: strain 945c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Caenargo, A.A.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Britones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Britones, M.R.S.; Bueno, M.R.P.; Faccincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Pocena, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi
Chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmineri, D.P.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anthranilate synthase component I XF1914 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Sate: 18-Aug-2000 *sequence_revision 20-Aug-2000 *text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Sató, S.; Kotaní, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasudd
DNA Res. 3, 109-115, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Accession: B82622
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 5
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Accession: S76994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: The genome sequence of the plant pathogen Xylella fastidiosa. Reference number: A82515; MUID:20365717; Reference number A59328 belince: for a complete list of authors see reference number A59328 belince:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
Superfamily: anthranilate synthase component I
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les 5; Conserv
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Pred. No.
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C;Superfamily: Pyrococcus
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A; Reference number: A75001
A; Accession: B75001
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Thes 5; Conserve
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A; Residues: 1-886 <BRO>
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A; Reference number: S48364
A; Accession: S48371
A; Nolecule fun-
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C; Superfamily: Saccharomyces cerevisiae hypothetical protein YIL073c
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superoxide dismutase (EC 1.15.1.1) (Fe) -
C;Species: Legionella pneumophila
                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Resdûdes: 1-149 <KAW>
A;Cross-references: GB:AJZ48288; GB:AL096836; NID:g5458960; PIDN:CAB50448.1; PID:g54:
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PAB1019 · Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
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    Mismatches

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Pred. No.
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Pred. No. 64;
1; Mismatches
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Pred. No. 2.4e+02;
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                     Legionella pneumophila
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submitted to JIPID, September 1992
A; Reference number: JS0749
A; Accession: JS0749
A; Molecule +---
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N;Alternate names: hypothetical protein o246
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: G65183; S30688
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C;Accession: JS0749
    C; Date: 16-J
C; Accession:
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A;Experimental source: strain Philadelphia-1
    ATP binding protein - Streptococcus gordonii
C;Species: Streptococcus gordonii
C;Dete: 16-7ul-1999 *sequence_revision 16-Jul-1999 *text_change 02-Sep-2000
C;Accession: T11549
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE000455; GB:U00096; NID:92367282; PIDN:AAC76801.1; PID:92367289; R;Experimental source: strain K-12, substrain MG1655 R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R. Scitence 257, 771-778, 1992 A;Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 the Reference number: S30660; MUID:92358234 R;Accession: S30688
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Best Local S
Matches 5
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; Residues: 1-192 < AME>
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NOte: the nucleotide sequence was submitted to the EMBL Data
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                      173 QEIIMR 178
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54 EEIIMK 59
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5; Conser
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                                                                                                                                                                                                                                 Conservative
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83.3%;
                                                                                                                                                                                                                                                  89.38;
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                                                                                                                                                                                                                               Score 25; DB Pred. No. 1.1e 1; Mismatches
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Pred. No. 84;
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Library, November 1992
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A;Gene: pol-r
A;Genome: mitochondrion
C;Keywords: mitochondrion
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A;Molecule type: DNA
A;Residues: 1-287 <KAW>
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A;Cross-references: GB:AJZ48283; GB:AL096836; NID:g5457433; A;Experimental source: strain Orsay C;Genetics: A;Gene: dppC-1; PAB0093 C;Superfamily: oligopeptide permease protein oppB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Kolenbrander, P.E.; Andersen, R.N.; Ganeshkumar, N.
Infect. Immun. 62, 4469-4480, 1994
A;Title: Nucleotide sequence of the Streptococcus gordon11 PK488 coaggregation adhes A;Reference number: 217283; MUID:95012638
A;Accession: T1549
                                                                                                                                    DNA polymerase homolog pol-r - rye mitochondr:
C;Species: mitochondrion Secale cereale (rye)
A;Variety: strain Halo
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-
C;Accession: S39814
R;Dohmen, G; Tudzynski, P.
Curr, Genet. 25, 59-65, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues; 1-251 (KOL>
A;Residues; 1-251 (KOL>
A;Cross-references: EMBL:L11577; NID:g310629; PID:g310631
A;Cross-references: strain PK488
A;Experiamily: short-chain AfP-binding cassette proteins;
F;29-221/Domain: ATP-binding cassette homology <ABC>
A;Molecule type: DNA
A;Residues: 1-289 <COH>
A;Residues: 1-289 <COH>
A;Cross-references: EMBL:X74132; NID:9439279; PIDN:CAA52229.1;
A;Experimental source: strain Halo; etiolated shoots
C;Genetics:
                                                                                 A; Title: A DNA-polymerase-related reading A; Reference number: S39814; MUID:94363738 A; Accession: S39814
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                                      PID: 9439280
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A;Gene: pol-r
A;Genome: mitochondrion
C;Keywords: mitochondrion
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A;Residues: 1-318 <HEI>
A;Residues: 1-318 <HEI>
A;Cross-references: GB:AE004111; GB:AE003852; NID:g9654614; PIDN:AAF93389.1;
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                  A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: G82350
                                                                                                                                                                                                                                                                                                                                                         R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 405, 477-483, 2000
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A;Experimental source: strain B-P2; etiolated shoots
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Ju
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Curr. Genet. 25, 59-65, 1994
A;Title: A DNA-polymerase-related reading A;Reference number: S39814; MUID:94363738
A;Accession: S39823
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R;Dohmen, G.; Tuo
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ip1d A biosynthesis lauroy1 acyltransferase VC0213 [imported] - Vibrio cholerae (strain):Species: Vibrio cholerae
;:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
;:Accession: G82350
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Best Local
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Residues: 1-312 <DOH>
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1 EEIIMR 6
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5; Conservative
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Pred. No. 1.3e
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Pred. No. 1.4e+02;
1; Mismatches 0;
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Pred. No. 1.4e+02;
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1.3e+02;
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F;131-139/Region: [F;443-471/Region: IF;538-545/Region: IF;538-545/Region: IF;152/Active site:
                                                                                                                                           C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C;Keywords: ATP; leucine zipper; nucleotide binding; P-loop; phosphotransferase F;123-371/Domain: protein kinase homology <KINP F;131-139/Region: protein kinase ATP-binding motif F;443-471/Region: leucine zipper motif F;443-471/Region: leucine zipper motif P;538-545/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U07358
A;Experimental source: brain
A;Experimental source: brain
A;Note: the nucleotide sequence for this amino acid sequence is inconsistent with th
he codon ACC for residue 661 as Pro, the codon GAACCACCTCCTCA for residues 664-668
C;Comment: This protein belongs to the family of non-receptor kinase.
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C; Superfamily: recN protein
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Biochem. Biophys. Res. Commun. 202, 613-620, 1994
B;Othem. Biophys. Res. Commun. 202, 613-620, 1994
A;Title: Cloning of a novel putative protein kinase having
A;Reference number: JC2363; MUID:94311945
A;Accession: JC2363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein kinase (EC 2.7.1.37) ZPK - human N;Alternate names: leucine-zipper protein kinase C;Species: Homo sapiens (man)
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C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C;Accession: F70350
C;Accession: F70350
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-668 < RED>
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A;Experimental source: strain VF5
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A; Residues: 1-520 <AQF>
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## ALIGNMENTS

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RESULT 2 SODF_LEGPN STANDARD; PRT; 192 AA. ID SODF_LEGPN STANDARD; PRT; 192 AA. AC P31108; DT 01-JUL-1993 (Rel. 26, Created) DT 01-JUL-1993 (Rel. 26, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DE SUPEROXIDE DISMUTASE [FE] (EC 1.15.1.1).	5; Conservative 1; Mi IMR 6 :   IMR 260	EMBL; 237997; CAA86097.1;  PIR; S48371; S48371.  SGD; S0001335; SP022.  Hypothetical protein.  SEQUENCE 886 AA; 102356 MW; 83084BC8D3C38945 CRC64;  SEQUENCE 886 AA; 102356 MW; 83084BC8D3C38945 CRC64;  SEQUENCE 883 AA; 102356 MW; 83084BC8D3C38945 CRC64;  SEQUENCE 883 AA; 102356 MW; 83084BC8D3C38945 CRC64;  SEQUENCE 883 AB; 102356 MW; 83084BC8D3C38945 CRC64;  SEQUENCE 883 AB; 102356 MW; 83084BC8D3C38945 CRC64;  SEQUENCE 883 AB; 102356 MW; 83084BC8D3C38945 CRC64;  SEQUENCE 885 AA; 102356 MW; 83084BC8D3C38945 CRC64;	opyright. It is prote of Bioinformatic street Bioinformatic street tutions as long as the is not removed. The agreement (See ht e agreement (See ht e agreement).	HYPOTHETICAL YIL073C. YIL073C. Saccharomyces Eukaryota; Fur Saccharomycet; NCBI_TaxID-49 [1]

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*Cloning and nucleotide sequences of iron and copper-zinc superoxide dismutase genes of Legionella pneumophila and their distribution among Legionella species ";

Jpn. J. Med. Sci. Biol. 49:167-186(1996).

-I- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.

-I- CATALYTIC ACCTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MSTLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., E
"Analysis of the Escherichia coli genome: DNA
from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                 01-Aug-1992 (Rel. 23, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-Aug-2001 (Rel. 40, Last annotation update)
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(UDP-MANNACA TRANSFERASE).
WECG OR RFFM OR B3794.
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METAL 27
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                                                                                                                                                                       NCBI_TaxID-562;
                                                                                                                                                                                                 Escherichia
                                                                                                                                                                                                                    Bacteria; Proteobacteria;
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E; PS00088; SOD_MN; 1
eductase: Tro
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Proteobacteria; q
aceae; Legionella
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                                                                                                                                                                                                                    subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                   246 AA
                             Blattner F.R.;
A sequence of the
                                                                                                                                                                                                                      Enterobacteriaceae;
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P42360;
01-NOV-1995 ()
01-NOV-1995 ()
01-OCT-1996 ()
HYPOTHETICAL
This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                  Kolenbrander P.E., Andersen R.N., Ganeshkumar N.;
"Nucleotide sequence of the Streptococcus gordonii pk488
"Nucleotide sequence of the Streptococcus gordonii pk488
"Infect. Immun. 62:4469-4480(1994).
"Infect. Immun. 62:4469-4480(1994)."
"INFERITY: BELONGS TO THE ATP-BINDING TRANSPORT PRO-
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CONFLICT 120
SEQUENCE 246 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-I- PATHWAY: INVOLVED IN THE SYNTHESIS OF ENTEROBACTERIAL COMMON
-NITIGEN (ECA) AND REQUIRED FOR SYNTHESIS OF LIPOPOLYSACCHARIDE O-SIDE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhev G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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                                                                                                                                                                                              MEDLINE-95012638; PubMed-7927711; Kolenbrander P.E., Andersen R.N.,
                                                                                                                                                                                                                            STRAIN-PK488
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                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
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246 AA;
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(Rel. 32, Last sequence update)
(Rel. 34, Last annotation update)
L ABC TRANSPORTER ATP-BINDING PROTEIN
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RESULT 5
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InterPro; IPR003493; ABC_transportr.
InterPro; IPR001489; ABC_TRANSPORTER;
InterPro; IPR001687; AFP_GTP_A.

Pfam: PP00005; ABC_tran;
ISMART; SM00382; AAA; 1.

PROSTTE; PS00211; ABC_TRANSPORTER; I.

PROSTTE; PS00211; ABC_TRANSPORTER; Transport.
Hypothetical protein; ATP-binding; Transport.
NP_BIND
46 53 ATP (POTENTIAL).
SEQUENCE 251 AA; 28054 MM; AED59C66F677D031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-93021519; PubMed-7935620;

IIVINE M. Hulma T., Prince A.M., Lustigman S.;

IIVINE M. Hulma T., Prince A.M., Lustigman S.;

"Identification and characterization of an Onchocerca volvulus c
clone encoding a highly immunogenic calponin-like protein.";

MOI. Biochem. Parasitol. 65:135-146(1994).

-!- FUNCTION: COULD BE INVOLVED IN MUSCLE CONTRACTION.

-!- TISSUE SPECIFICITY: FOUND IN THE LONGITUDINAL MUSCLES BELOW.
                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bloinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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NCBI_TaxID=6282;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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01-FEB-1996 (Rel.
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                                                                                                                     REPEAT
REPEAT
REPEAT
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IN MISCELLANEOUS: THERE ARE APPARENTLY SEVERAL FORMS OF THE NATIVE PROTEIN WHICH APPEAR TO BE EXPRESSED IN A STAGE-SPECIFIC MANNER.

IN SMILARITY BELONGS TO THE CALPONIN FAMILY.

IC CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-22 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                      EMBL; U01099; AAA20215.1; ALT_SEQ.
InterPro; IPR000557; Calponin_repeat.
Pfam; PF00402; calponin; 7.
                                                                                                  SEQUENCE
                                                                                                                                                                                                    REPEAT
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63;
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         007994;
007994;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last sequence update)
30-MAPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) (P450R).
Musca domestica (House fly).
Musca domestica (House fly).
Peukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Metazoa; Endopterygota; Diptera; Brachycera; Muscoldea; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02483; SMC_C; 1.

Pfam; PF02483; SMC_C; 1.

DNA repair; ATP-binding; Complete proteome.

ATP (POTENTIAL).

PARA 60439 MW; A9708562ACBE901E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000695; AAC06789.1; -.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003405; SMC_C.
Pfam; PF02483; SMC_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98196666; PubMed-9537320; Deckert G., Warren P.V., Gaasterland T., Young W.G., Ler Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001
20-AUG-2001
20-AUG-2001
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RECN OR AQ_561.
Aquifex aeolicus.
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NCBI_TaxID=63363;
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SIMILARITY: BELONGS TO THE RECN FAMILY.
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83.3%;
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(RECOMBINATION PROTEIN
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Pred. No.
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                                                            Brachycera; Muscomorpha;
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A Koener J.F., Learner A. Koener J.F., Learner A. The cDNA and deduced protein sequence L. The color and deduced protein sequence L. The color and deduced protein sequence L. The color and the color of the color o
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HSER_C/
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Best Local S
Matches 4
HSR_CAVPO STANDARD;

HSR_CAVPO STANDARD;

P70106;

P70106;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

HBAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL GLANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR) (GUANYLYL CYCLASE (GUCYZC OR GUCZC.

Cavia porcellus (Guinea pig).

TOWATVOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _CAVPO
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HSSP: P00388; IAMO.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdxn-like.
InterPro; IPR001709; Flavpyrid_cyt_redctse.
InterPro; IPR0017433; Oxidored_FAD.
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STRAIN=RUTGERS; TISSUE=Abdomen;
MEDLINE=93284260; PubMed=8508186;
MEDLINE=93284260;
MEDLINE=9328426
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Pfam; PF00175; oxidored_fad; 1
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Pred. No. 1.2e+02;
2; Mismatches 0;
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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SEQUENCE FROM N.A.
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EMBL; 274734; CAA98989.1; -.
HSSF; 002846; 1AML.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0001054; Guanylt_cyclase.
pfam; pF01094; ANF_receptor; I.
pfam; pF00211; guanylate_cyc; 1.
pfam; pF00069; pkinase; 2.
pfam; pF00069; pkinase; 2.
pham; pR00694; CYCC; 1.
procerp.
ELYS_HALKA STANDARD; PRT; 154 AA (201382; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-FEB-1995 (Rel. 31, Last annotation update) EGG-LYSIN PRECURSOR (SPERM-LYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2; PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kruhoeffer M., Cetin Y., Kaempf U., Forssmann W.-G.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ dehases.
-I-FUNCTION: RECEPTOR FOR THE B. COLI HEAT-STABLE ENTEROTOXIN (E.COLI ENTEROTOXIN MARKEDLY STINULATES THE ACCUMULATION OF CGMP IN MANMALIAN CELLS EXPRESSING GC-C). ALSO ACTIVATED BY THE ENDOGENOUS
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CATALITIC ACTIVITY: GTP = 3,'5'-CYCLIC GMP + PYROPHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Lyase; cGMP synthesis; Signal
                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                        Pred. No. 1.9e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUANYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAT-STABLE ENTEROTOXIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                 DB 1; L.
1.9e+02;
0;
                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --
                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                               Length 1076;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration - MBL outstation
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RESULT 10
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   RP SEQUENCE FROM N.A.

RR SETABLEGER A.F., STRAUBINGER R.K.;
RS SETABLEGER A.F., STRAUBINGER R.K.;
RS SUBMILLEGE (FEBS-1998) to the EMBL/GenBank/DDBJ databases.

RL SUBMILLEGE (FEBS-1998) to the EMBL/GenBank/DDBJ databases.

RL SUBMILLEGER (FEBS-1998) to the EMBL/GenBank/DDBJ databases.

RC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STEULATES

CC HATURATION & PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL

CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMANTORY RESPONSE, BEING

CC IDENTIFIED AS ENDOGROUS PROGENS, AND ARE REPORTED TO STIMULATE

CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS

CC (BY SIMILARITY).

CC -!- SUGUNIT: MONOMER (BY SIMILARITY).

CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

CC -!- MIGGELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEMENT IN THE

CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                 046612;
15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by positive Darwinian selection.";
Biol. Bull. 182:97-104(1992).
FUNCTION: DISSOLVES THE EGG VITELLINE LAYER NONENZYMATICALLY
DURING FERTILIZATION. IT CREATES A HOLE OF ABOUT 3 MU-M IN
DIAMETER THROUGH WHICH THE SPERM PASS.
-1- SUBUNIT: HOMODIMER.
-1- TISSUE SPECIFICITY: SPERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haliotis kamtschatkana (Pinto
Eukaryota; Metazoa; Mollusca;
Haliotidae; Haliotis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001379; Egg_lysin. Pfam; Pf01303; Egg_lysin; 1. ProDom; PD002750; Egg_lysin; 1. Fertilization; Sperm; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M59970; AAA29200.1; -. HSSP; P04552; 1LYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    Canis familiaris
                                                                                                                                                                                                                                                      NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                   NTERLEUKIN-1
                                                                                                                                                                                                                                                                                                                                                                                                               L1A_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEIIMR
||||:|
39 EEIIVR
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divergence of sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial is requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 83. 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 AA;
                                                                                                                                                                                                                                                                                                                              (Rel. 37
(Rel. 37
(Rel. 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
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                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                             (Dog).
oa; Chordata; Craniata; Ver
ia; Carnivora; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                37, Created)
37, Last sequence up
37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         species-specific
                                                                                                                                                                                                                                                                                                                                PRECURSOR (IL-1 ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18386 MW;
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D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGG-LYSIN.
; 8875D2B9E6CF3564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abalone).
Gastropoda; Archaeogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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43;
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la; Canidae;
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                                                                                                                                                                                                                                                                         Euteleostomi;
Canis.
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RESULT 11

ARCC_HELPY
ID ARCC_YELPY
ID ARCC_YELPY
ID ARCC_YELPY
ID ARCC_YELPY
ID O1-NOV-1997
DT 01-NOV-1997
DT 01-NOV-1997
DT 02-AUG-2001
DE CHORISMATE;
DE PHOSPHOLYAS
GN ARCC OR HPO
OS Helicobacte
OC Helicobacte
OC Helicobacte
OC Helicobacte
OC HELICOBACTE
OC STRAIN=2669
RC STRAIN=1068
RA MEDLINE-973
RA LOFTUS B.,
RA LOFTUS B.,
RA COTCON M.).
RA HAYES W.S.,
RA COTCON M.).
RA VENTE J.C.
RA NEULT 388:
CC -1- CATALYT
CC TIB BIO
CC -1- COPACTO
CC -1- SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFT THE CONTRACT OF THE CONTR
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
PHOSPHOLYASE).
AROC OR HP0663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0264; INTERLEUKIN1.
SMART; SMO0125; ILL; 1.
PROSITE; PS00253; INTERLEUKINTO
Cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF047011; AAC03066.1; -
InterPro; IPR000975; Interleukin_1.
InterPro; IPR003502; Interleukin_1_prop.
Pfam; PF00340; IL1; 1.
Pfam; PF02394; IL1_propep; 1.
STRAIN-26695 / ARCC 700392;
STRAIN-26695 / ARCC 700392;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Relson K., Ouackenbush J., Zhou L., Kirness E.F., Peterson S.,
Nelson K., Ouackenbush J., Zhou L., Kirness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., Fitzgerald L.M., Fulli C., Bowman C., Watthey L., Wallin E.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori (Campylobacter Bacteria; Proteobacteria; epsilon s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                             /enter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEVIMK 106
                                                                                                                                                                                                                                           complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macrophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
98
137
265 /
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137
30521
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKIN-1 ALPHA.

N-LINKED (GLCNAC. . .) (P.

N-LINKED (GLCNAC. . .) (P.

CC1D316CA37173A8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r pylori).
subdivision;
                                                                                                                                                                                                                                                  gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365
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77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                  pathogen Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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INP_BOVIN

INP_BOVIN

P2132;

01-MAY-1991 (Rel. 18, Created)

T 01-MAY-1991 (Rel. 18, Last sequence update)

T 20-AUG-2001 (Rel. 40, Last anotation update)

T 20-T 20-T Rel. 40, Last anotation update)

T NOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 5
                                                                              BIOCHEMISTRY 33:13164-13171(1994).

11 CATALYTIC ACTIVITY: D-MYO-INOSITOL 1,4-BISPHOSPHATE + H(2)O-THOSITOL A-PHOSPHATE + ORTHOPHOSPHATE.

12 CHARACTER REGULATION: INHIBITED BY LI(+).

13 CHARACTER PHOSPHATIDYL INOSITOL SIGNALING PATHWAY.

14 SUBUNIT: MONOMER.

15 SUBUNIT: MONOMER.

16 MISCELLANEOUS: ACTS ON INOSITOL 3,4-BISPHOSPHATE AND INOSITOL 1,3,4-TRIPHOSPHATE (FORMING INOSITOL 3,4-BISPHOSPHATE) WITH TIMES HIGHER AFFINITY FOR THE BISPHOSPHATE.

17 SIMILARITY: BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 12
BOVIN
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                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-95034747; PubMed-7947723;
York J.D., Ponder J.W., Chen Z.W., Mathews F.S., Majerus P.W.;
"Crystal structure of inositol polyphosphate 1-phosphatase at 2.3-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                  YOR J.D., Majerus P.W.;
"Isolation and heterologous expression of a cDNA encoding inositol polyphosphate 1-phosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 87:9548-9552(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyase; Aromatic SEQUENCE 365 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91088555; PubMed=2175905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodom; PRO1284; Chorismate_synt; 1.

Prodom; PRO02941; Chorismate_synt; 1.

PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.

PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.

PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.

PROSITE; PS00789; CHORISMATE_SYNTHASE_3; Complete proteome.

Lyase; Aromatic amino acid biosynthesis; Complete proteome.

SEQUENCE 365 AA; 40100 MW; 98ABC708E1909561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287
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les 5; Conserv
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EEIIVR 292
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1264; Chorismate_synt; 1.
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83.3%;
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1; Mismatche
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(EC 3.1.3.57) (IPPASE) (IPP).
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1.1e+02;
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EMBL; U07951; AAB16908.1; HSSP; P21856; IGND. MGD; MGI:99845; Gd12.

InterPro; IPR002005; Rab_GDI_REP.
Pfam; PF00996; GDI; 1.
PRINTS; PROCOCO.

GTPase activation. SEQUENCE 445 AA; PRINTS; PR00891; RABGDIREP PRINTS; PR00892; RABGDI.

50512 MW;

7FFD92EAE950EE49 CRC64;

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Matches 5
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PIR; A39254; A39254.
PDB; IINP; 26-JAN-95.
InterPro; IPR000760; Inositol_P.
Pfam; PF00459; inositol_P; 1.
PRINTS; PR00378; INOSPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, 20-AUG-2001 (Rel. 40, 20-AUG-2001 (Rel. 40, RAB GDP DISSOCIATION 1 GDI2 OR RABGDIB.
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P50397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restricted the companion of the companion 
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metharia; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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CONFLICT 84 84 L ->
SEQUENCE 400 AA; 43931 MW; CF
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40, Last sequence update)
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10N INHIBITOR BETA (RAB GDI BETA) (GDI-2).
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Pred. No. 1.2e+02;
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Sciurognathi; Muridae;
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CF385265E4C674AA CRC64;
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; Murinae; Mus
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RESULT

256 EETIMO 261

1 EEIIMR 6

Query Match Best Local S Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fanning S., Leahy M., Sheehan D.;
"Nucleotide and deduced amino acid sequences of Rhizobium meliloti
102F34 lacz gene: comparison with prokaryotic beta-galactosidases human beta-glucuronidase.";
Gene 141:91-96(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BGAL_RHIME STANDARD; PRT; 755 AA. 059750; C59750; T5-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 15-DEC-1998 (Rel. 37, Last annotati
ENV_HVIND STANDARD; PRT; 846 AA. P1879; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-JUL-1990 (Rel. 38, Last annotation update) ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L20757; AAA26296.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94215895; PubMed=8163182; Fanning S., Leahy M., Sheehan D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCIN GALACTOSE RESIDUES IN BETA-D-CALACTOSIDES. SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 83. 5; Conservative
                                                                                                                                                                                                                                                                     Similarity 66. 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IPRO1649; Glyco_hydro_2.

10703; Glyco_hydro_2: 1.

PS00719; GLYCOSYL_HYDROL_F2_1;

PS00608; GLYCOSYL_HYDROL_F2_2;
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463 N
84148 MW;
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83.3%;
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Pred. No. 2.4e
2; Mismatches
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Pred. No.
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NUCLEOPHILE (BY SIMILARITY).
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"Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the human immunodeficiency virus.";
Gene 81:275-284(1989).
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotei
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PIR; JQ0066; VCLJND.
HIV: M27323; ENV$NDK.
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NCBI_TaxID=11695;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                              Polyprotein; Glycoprotein; Transmembrane;
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TRANSMEMBRANE GLYCOPROTEIN.
BY SIMILARITY.
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SEQUENCE NCBI_TaxID=382;

RESULT 15
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Query Match Best Local S Matches 4

551

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Hydrolase;
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PF00703;

Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 263 EEIIIR 268

Search completed: March 18, 2002, 09:52:28
Job time: 297 sec

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    of hits satisfying chosen parameters:
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O70481 mus musculu
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01-MAR-2001 (TIEMBLrel. 16, Created)
01-MAR-2001 (TIEMBLrel. 16, Last sequence update)
01-MAR-2001 (TIEMBLrel. 16, Last annotation update)
01-MAR-2001 (TIEMBLREL. 16, Last annotation update)
CDNA FLJ12968 FIS, CLONE NTZRP2005815.
HOMO SAPLENS (HUMAD).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      LIGASE E3-ALPHA).
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## ALIGNMENTS

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Query Match
Best Local Similarity 83:
Matches 5; Conservative
070481 PRELIMINARY;
070481;
01-AUG-1998 (Tremblrel. 07, C:
01-AUG-1998 (Tremblrel. 07, Li
01-JUN-2001 (Tremblrel. 17, Li
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N-end rule pathway.";
Submitted (MAY-1998) to the EMBL/GenB EMBL; AF067379; AAC33678.1;
EMBL; AF067371; AAC33678.1; JOINED EMBL; AF067372; AAC33678.1; JOINED EMBL; AF067373; AAC33678.1; JOINED EMBL; AF067374; AAC33678.1; JOINED EMBL; AF067375; AAC33678.1; JOINED EMBL; AF067376; AAC33678.1; JOINED EMBL; AF067376; AAC33678.1; JOINED EMBL; AF067376; AAC33678.1; JOINED EMBL; AF067377; AAC33678.1; JOINED EMBL; AF067378; AAC33678; AAC33678; AAC33678; AAC3478; AA
SEQUENCE FROM N.A.

STRAIN-DELTA H;

MEDLINE-9937514; PubMed-9371463;

MEDLINE-99307514; PubMed-9371463;

MITHOUSE T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,

McDougall S., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
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                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
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Mammalia; Eutheria;
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N.G., Jenkins N.A., Varshavsky A.;
genes encoding the recognition component
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01-NOV-1996
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Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                    Synechocystis sp. strain PCC6803 entire genome and assignment of DNA Res. 3:109-136(1996). EMBL, D64005; BAA10686.1; ---
EMBL, D64005; BAA10686.1; ---
SEQUENCE 263 AA; 28752 MW; 2
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MEDLINE-96127529; pubMed-8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Mi
Sugiura M., Tabata S.;

"Sequence analysis of the genome of the unicellular cya
Synechocystis sp. strain PCC6803. I. Sequence features
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                             SPY1012
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EMBL; AE000884; AAB85637.1; -.
Complete proteome.
SEQUENCE 157 AA; 17145 MW; 7EA
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MEDLINE-97061201;
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    group; Streptococcaceae;
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.C.,
RA Coutinho L.L., Cristofani M., Diss.Neto E., Docena C., El-Dorry H.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Kuramae E.B., Laigret F., Losta M.C.R., Kitalima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Marques M.V., Marcins E.A.L., Madeira H.M.F., Machado J.A.,
RA Marques M.V., Marcins E.A.L., Martins E.M.F., Machado J.A.,
RA Marques M.V., Marcins E.A.L., Martins E.M.F., Machado J.A.,
RA Manda M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Peixoto B.R., Pereira G.A.G., Pereira N.A.,
RA Peixoto B.R., Pereira G.A.G., Pereira D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira D.A., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Silveira J.F., Silveira M.G., de Forter M.J.,
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STRAIN-SF370;

MEDLINE-21192684; PubMed-11296296;

MEDLINE-21192684; PubMed-11296296;

MEDLINE-21192684; PubMed-11296296;

MEDLINE-21192684; PubMed-11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K., Ferretti J.J., McShan W.M., Ajdic D.J., Kenton S., Lai H.S., Lin S.P., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

BMBL; AE006546; AAR33910.1;

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ANTHRANILATE SYNTHASE COMPONENT I
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Best Local
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"Serologic and molecular screening for Ntcheu, Malawi: high prevalence of H)
hepatitis B and C viruses.";
Submitted (SEP-2000) to the EMBL/Geni EMBL; AF309426; AAG49507.1;
NON_TER 1 1
NON_TER 71 71
NON_TER 71 AA; 7927 MW; 3DDBA8E1
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099F59;
01-JUN-2001
01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                            O73207 PRELIMINARY; PRT; 81 AA.
073207;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                 Roques P.;
Submitted (MAY-1998) to the
EMBL; AJ006737; CAA07211.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
                                                                                                                                                                SEQUENCE FROM
STRAIN-SAMPLE
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Viruses; Retroid viruses; Retroviridae;
NCB_TaxID=11676;
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     Envelope protein.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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CAMOO1B;
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83.3%;
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Pred. No. 4.7e
1; Mismatches
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                                                                                                                         EMBL/GenBank/DDBJ
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. 4.7e+02;
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1.1e+02;
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01-MAY-2000 (
01-JUN-2001 (
GLYCOPROTEIN :
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                                  "Highly variable sequences at env V3 region of among Thai carriers during 1995 to 1997."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ dEMBL: AB031954; BAA83904.1; -. InterPro; IPR000777; GP120. Pfam: PF00516; GP120: 1.
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-97RVT592;
STRAIL W., Ayuthaya P.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus Viruses; Retroid viruses; Re
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STRAIN-95TNIH322;
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae;
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LN 120 (FRAGMENT).
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(TYEMBLrel. 13, Last sequence update)
(TYEMBLrel. 17, Last annotation update)
video (FRAGMENT).
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Retroviridae;
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1.5e+02;
hes 0; Indels
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1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lentivirus
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                                                                                                                                                                                                                                                                                                              Mukai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                     HIV-1
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Best Local S
Matches 5
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9YN32 PRELIMINARY;
Q9YN32;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-JUN-2001 (TrEMBLrel. 17, L
ENVELOPE GLYCOPROTEIN GP120 (
                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SUBTYPE E.
Sato H., Shiino T., Kodaka N., Taniguchi K., Tomita
Sato H., Shiino T., Kodaka N., Taniguchi K., Tomita
Miyakuni T., Takebe Y.;
Miyakuni 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9E4C3 PRELIMINARY; PRT; 102 AA.
Q9E4C3;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TREMBLREL. 17).
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leroux C.;
"HIV-1 shedding.";
"Bubmitted (APR-2000) to the Submitted (APR-2001) to the SMBL; AF256402; ARG16123.1;
Envelope protein.
                                                                        InterPro; IPR000777; ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
NON_TER 1 1
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STRAIN-PATIENT 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1,
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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||||:|
2 EEIILR 7
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EEIILR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 AA;
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10795 MW;
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Last sequence up
Last annotation
(FRAGMENT)
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1; Mismatches
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Pred. No. 1.6e
1; Mismatches
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1.6e+02;
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1.5e+02;
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Gaps

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Kato K.,

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RESULT 14
Q9E4F8
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Best Local S
Matches 5
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Best Local Similarity 83.
Matches 5; Conservative
Query Match
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "HIV-1 shedding.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
EMBL; AF256426; AGG16087.1;
InterPro; IPRO00777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-PATIENT 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID-11676;
                                                                                                                                                                                                                                                                                           Q9E4F8
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01-MAR-2001 (TEBMBLrel. 16, Last sequence update)
01-JUN-2001 (TEBMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                            "HIV-1 shedding.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF256427; AAG16088.1; -.
InterPro; IPR000777; GF120.
Pfam; PF00516; GP120; 1.
                                                                                                                                      SEQUENCE FROM N.A. STRAIN-PATIENT B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                        fuman immunodeficiency virus type 1.
/iruses; Retroid viruses; Retroviridae;
vCBI_TaxID=11676;
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||||:|
14 EEIILR 19
                                                                                                                                                                                                                           1-MAR-2001 (TrEMBLrel. 16, Created)
11-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-UN-2001 (TrEMBLREL. 17, Last annotation update)
NVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                              9E4F8;
                                                                                                                                                                                                                                                                                                                                                        2 EEIILR 7 '
                                                                                                                                                                                                                                                                                                                                                                               1 EEIIMR 6
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5; Conserv
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107 AA;
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                                    107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
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12305
                                      12032 MW;
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  89.38;
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Pred. No. 1.7e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 12; Length 107; Pred. No. 1.7e+02; 1; Mismatches 0; Indels
  Score
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1600A374D8ED6F51 CRC64;
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                                      2E274D8528E39E9E CRC64;
  25;
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                                                                                                                                                                                           Lentivirus
  DB 12;
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  Length 107;
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Query Match
Best Local Similarity
Watches 5; Conserve
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Search completed: March 18, 2002, 09:51:59
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                                                                                                                                                                                                                                     Leroux C.;
"HTY-1 shedding.";
"bubmitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AP256430; AAG16091.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9E4F5 PRELIMINARY; PRT; 107 AA.

Q9E4F5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCDI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-PATIENT 8;
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                                                                                                     1 EEIIMR 6
                                                                                                                                                                                                             107 AA; 12065 MW;
                                                                                                                                      Conservative
                                                                                                                                                  89.38;
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1; Mismatches 0;
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Pred. No. 1.7e+02;
                                                                                                                                                                                                               1600A374D8ED6F51 CRC64;
                                                                                                                                      Mismatches
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                                                                                                                                                                 Length 107;
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